STIC-Biotech/ChemLib

From: Sent: To:

Yu, Misook

Subject:

Wednesday, August 28, 2002 8:35 AM STIC-Biotech/ChemLib 09/900,147

Please search SEQ ID NO:1

Examiner Misook Yu, Ph.D. 703-308-2454 (Phone) Art Unit 1642 CM1-8E18 (Room) CM1-8E12 (Mail Box)

Edward Hart Technical Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

All Slanch here

| | TYPE OF SEARCH: | VENDOR/COST (where applic.) |
|-----------------------|-----------------|-----------------------------|
| Searcher: | NA Sequences: | STN: |
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| Location: | Structures: | Questel/Orbit: |
| Date Picked Up: | Bibliographic: | DRLink: |
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044080 drosophila
09v6m0 drosophila
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09v6m2 drosophila
091624 arabidopsis
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O1-DEC-2001 (TrEMBLrel. 1
TRANSCRIPTION PACTOR DP 1
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Eukaryota: Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxID=10090;
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Opbz44 homo sapian
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Opfra8 arabidopsis
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RX MEDLINE-2108566; PubMed-11217851;

RX MEDLINE-2108566; PubMed-11217851;

RA ALENAMA T. HARA A., Shibata R., Yoshino M., Itoh M., Ighii Y.,

RA ALENAMA T., HARA A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA ALENAMA T., HARA A., Fukunishi Y., Konno H., Koaukawa T., Salto R.,

RA ALENAMA T., HARA M., Sishi R., Kiyosawa H., Rondo S., Tamanaka I.,

RA ALENAMA R., ISANA Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

RA ALENAMA R., HARA M., Salto T., Giasi C., Ring B., Kophiva H.,

RA Flaischmann W., Gassterland T., Giasi C., Ring B., Kophiva H.,

RA Halsenhmann W., Gasterland T., Washer L., Washio T.,

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RA Schrimi L.M., Staubli F., Suzuli R., Tomita M., Wagner L., Washio T.,

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RA Gustincich S., Hill D., Mashima J., Mazzarelli J., Mombaerts P.,

RA Hordnone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,

RA Hordnone P., Scorch R., Wang K., Waltz C., Whittaker C., Wilming L.,

RA Hynshaw-Boris A., Yoshida K., Hasegawa T., Kamiya H., Kohteuki S.,

RA Haveshiaki Y., Schochbach C., Seya T., Shibaca T., Kohteuki S.,
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   09UG28;
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**RABLE 409:688-690(2001).

**EMBL; AK019997; BAB31959.1; -.

**HSSP: Q14188; 1CF7.

**HSSP: Q14188; 1CF7.

**INCOLUMN TIPE 1.

**INCOLUMN TIPE 1.

**Fam: PP03119: E2F_TDP: 1.

**SEQUENCE 396 AA; 43804 MM; 392AE2ED28165621 CRC64;
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Eukaryota; Metazoa;
Mammalla; Eutherla;
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Interpro; IPRO03316; E2F_TDP.
Pfam; PPO0319; E2F_TDP; 1.
SEQUENCE 290 AA; 32494 MV; AA3079A6FC4F1DD0 CRC64;
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Pred. No. 4.9e-18;
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Pred. No. 3.5e-18;
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
DN FACTOR DP (FRAGMENT).
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Query Match 90.3%;
Best Local Similarity 88.9%;
Matches 32; Conservative
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Best Local Similarity 100.0%;
Watches 37; Conservative C
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01-DEC-2001 (TERMBLES). 19, Las
TRANSCRIPTION FACTOR DP1.
Brugia malayi.
Eukaryota Hetazoa; Nematoda; C
Onchocercidae; Brugia.
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01-MAY-2000 (TrEMBLiel. 13, Last sequence up
01-JUN-2001 (TrEMBLIEL. 17, Last annotation
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DRFLP4346232.
                                                               *Brugia melayi DP1 transcription factor.*;

Summitted (JUL-2000) to the EMBL/GenBank/DOBJ databases.

EMBL, AP28430; AAC1473-1; -.

HSSP; Q14188; ICP7.

InterPro; IR093316; E2F_TDP.

Pfam; PP0319; E2F_TDP; 1.

SEQUENCE 381 AA; 43534; MN; 63PE58P7D4FD76E5 CRC64;
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SEQUENCE 416 AA; 4
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                SEQUENCE FROM N.A.
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Pfam; PF02319; E2F_TDP; 1:
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Primates;
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AC QSYGNO; O17472;
DT 01-MAY-2000 (TERMEIFEL 13, Created)
DT 01-MAY-2000 (TERMEIFEL 13, Last sequence update)
DT 01-JUN-2001 (TERMEIFEL 17, Last annotation update)
DT DRIBE PRODUCT (TEANSCRIPTION PACTOR E2F DP SUBUNIT).
DP GENE PRODUCT (TEANSCRIPTION FACTOR E2F DP SUBUNIT).
OB DR CG4654.
OB DR OR CG4654.
OB DROSOPHILA melanogaster (Fruit fly).
OC ENERTYOLS; Metazos; Arthropoda; Trachesta; Hexapoda; Insecta;
OC Ptergoca; Neoptere; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroides; Drosophilidae; Drosophila.

NCBI_TaxID-7227;
NCBI_TaxID-7227;
RX Adams M.D. (Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.
RA Amanatides P.G., Scharer S.E., Li P.W., Hoskins R.A., Galle R.F.
RA Mannatides P.G., Scharer S.E., Li P.W., Hoskins R.A., Galle R.F.
RA Amanatides P.G., Scharer S.E., Li P.W., Hoskins R.A., Galle R.F.
RA Aberia R.A., Lavis S.E., Richards S., Ashburing, M., Henderson S.N.,
RA Sutton G.G., Wortnan J.R., Yandell M.D., Zhanga, M., Chan L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Ashbyani A., An H. J., Andrews Pfennkoch C., Miklos G.L.G.,
RA Abril J.F., Ashbyani A., An H. J., Andrews Pfennkoch C., Baldwin D.,
RA Abliew R.M., Besu A., Bexendale J., Bayrakteroglu L., Bessley E.M.,
RA Beson K.F., Benos P.V., Berman B.F., Bhandari D., Botishakov S.,
RA Bertis R.C., Busham D.A., Butler H., Cadisu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherris R.C., Busham D.A., Deng I., Mays A.D., Dev II., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.M., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Raipen G.H., Ke I., Kennison J.A., Katchum K.A.,
RA Alali H., Kalush F., Karpen G.H., Ke I., Kennison J.A., Katchum K.A.,
RA Alanko P., Lei Y., Levitsky A.A., Li J., Li I., Ling Y., Lin X.,
RA Hount S.M., Holy M., Hurphy E., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Nelson M., Pittman G.S., Pan S., Pollard J., Puri V., Reese H.G.,
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Best Local Similarity 86.1%;
Marches 31; Conservative
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EMBL; APO1152; AA887765.1; ...
HSSP; 014188; LCP7.
F1yBase; FBgn0011763; Dp.
InterPro; IPR003316; E2E_TDP.
Pfam; PF02119; E2E_TDP; 1.
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
MCBI_TaxID=7227;
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STRAIN-BERKELEY;
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Pred. No. 3e-15;
4; Mismatches 1
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X MEDLINE-98078671, PubMed-9418862;

X MEDLINE-98078671, PubMed-9418862;

A Duronio R.J., Bonnette P.C., O'Farrell P.H.;

Y MULATIONS Of the Drosophila dDP, dE2F, and cyclin E genes reveal distinct roles for the E2F-DP transcription factor and cyclin E during the G1-S translition.";

Y Distinct roles for the E2F-DP transcription factor and cyclin E during the G1-S translition.";

X HOL. Cell. Biol. 18:111-151(1998).

X EBUL, AF003819; AFF08403-1; -.

X EMBL; AF031700; AAC02971.1; -.

X HSSP; Q14188; 1CF7.

X HSSP; Q14188; 1CF7.

X PIPBASC; FB900011763; DP.

X PIPBASC; FB900011763; DP.
    Query Match
Best Local S
Matches 33
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Best Local Similarity 85.1
Matches 31: Conservative
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OSNESA (TESMBLTel, 1
O1-OCT-2000 (TESMBLTel, 1
O1-OCT-2000 (TESMBLTel, 1
O1-DEC-2001 (TESMBLTel, 1
E29-LIKE PROFEIN.
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The genome sequence of broapphila melanogaster.*;
Science 287:3185-2195(2000).
                                                                                                                                                                                                                                                                                                                               #CA661.

Homo sepiens (Human).

Eukaryota: Hetasca; Chordata; Craniata; Vertebrata; Euteleostomi;

Hommalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                        Pand X., Vaughon H., Chen W., StClair F., Han K., Cebon J.;
"Cioning and character#gation of novel genes related to hepatocellular carcinoma.";
submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF219119; AR277562.1;
HSSP; O14188; ICF7.
HSSP; O14188; ICF7.
InterPro; IPRO316; EZF-TDP.
InterPro; IPRO316; EZF-TDP.
SEQUENCE 233 AA; 26053 MM; CSF9F8D2B75E4784 CRC64;
                                                                                                                                                                                                                                                              SEQUENCE PRON N.A.
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Similarity 85.5%;
32; Conservative
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: Score 164; DB
; Pred. No. 3.6e
3; Mismatches
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Last sequence update)
Last annotation update)
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Pred. NO. 3.7e-15;
4; Mismetches 1
DB 4:
3.6e-15;
2;
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                                      Length 233;
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Best Local S
Natches 30
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Best Local Similarity 83.3%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    thaliana.";
thaliana.";
FBBS Lett. 486:79-87(2000).
EMBL; AJ394532; CAC15484.1;
EMSSP; Old1884 [EF7.
INTERPRO] IPRO03316; E2F_TDP.
R PÉMB; PF03319; E3F_TDP; 1.
R PÉMB; PF03319; E3F_TDP; 1.
SECUTENCE 385 AA; 42755 MM; 51
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OSENY2;

O1-MAR-2001 (TrEMBLrel. 1

O1-MAR-2001 (TrEMBLrel. 1

O1-DEC-2001 (TrEMBLrel. 1

DP-LIKE PROTEIN.
                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicota; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TexID-3703;
                                                                                                                                                   SEQUENCE FROM N.A.
Bevan M., Pohl T., Weizenegger
Lembke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMF
                                                                                                                                                                                                        P1384_160.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; cgre eudicots; Rosid
euromids II; Brassicales; Brassicaceae; Arabidomois.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-20562805; PubMed-11108847;
MAGYAR E., Atanassovs A., de Veylder L., Rombauts S., Inze D.;
"Characterization of two distinct DP-related genes from Arabidopsis
                                                                       HSSP: Q14188; ICF7.
InterPro; IPR003316; E2F_TDP.
Pfom; PF02319; E2F_TDP; 1.
SEQUENCE 413 AA; 45604 MW;
                                                                                               EU Arabidopsis sequencing pr
Submitted (MAR-2000) to the
EMBL: AL162751; CAB83299.1;
MSSP: Q14188; ICF7.
                                                                                                                                                                                                 MCBI_TaxID-3702;
                                                                                                                                      EQUENCE FROM N.A.
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                             y Match 81.2%;
Local Similarity 83.3%;
hes 30; Conservative
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16, Last sequence update)
19, Last annotation update)
                                                                                                                             project;
                             Score 151; DB 10;
Pred. No. 4.5e-13;
3; Mismatches 3;
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Pred. No. 4.1e-13;
3; Wismatches 3;
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                                                                                                                   EMBL/GenBank/DDBJ
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                                                                        239FDC6DAED2F7:23
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                                                                          CRC64;
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   Query Match
Best Local Similarity
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                                     Ligane.
SEQUENCE
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Query Match 73.1%;
Best Local Similarity 75.8%;
Matches 25; Conservative
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EU Arabidopois sequencing project;
Submitted (APR-2000) to the EMBL/Gen
EMBL; ALL62971; CABB9984 1; ~.

HSSP; O14188; LCF7.

InterPro; IPRO03316; E2F_TDP,
Pfam; PP02319; E3F_TDP; 1.

SEQUENCE 288 AA; 12560 MM; ECOAD
                                                                                                                                                                                                                                                                                        Arabidopais thaliana (Mouse-car cress).

Sukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Sparmatophyta; Magnoliophyta; endicotyledona; core endicota; Rosidae;

eurosida II; Brasaicalega Brasaicaceae; Arabidopsis.

MCBI_TaxID-3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Sparmatophyta; Magnoliophyta; eudicotyledona; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-OCT-2000 (TrEMBLTel. 15, Lac
01-DEC-2001 (TrEMBLTel. 19, Lac
DP-2 TRANSCRIPTION FACTOR-LIKE
                                    FEBS Latt. 486:79-87(2000).
EMBL, A7294531; CAC14483.1; -
HSSP; O14188; 1CF7.
InterPro; ITRO03316; E2F_TDP,
Pfam; PF03319; E2F_TDP; 1.
                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-20502803; PubMed-11108847;
Maysar E., Kansasova A., de Veylder L., Rombauts S.,
"Characterization of two distinct DP-related games fro
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLIE). 16, Created)
01-MAR-2001 (TrEMBLIE). 16, Last sequence update)
01-DEC-2001 (TrEMBLIE). 19, Last annotation update)
DP-LIKE PROTEIN (EC 6.3.2.19)
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33038 MW;
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CRC64;
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Score.

136; DB 10; No. 4.1e-11;

Length 292,

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RESULT
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Best Local 5
Matches 24
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Query Match
Best Local Similarity
                                                                       Ceol C. J., Horvitz H. R.;

'QD1 1 DP and ef1-1 E2F Act with lin-35 Rt
in C. elegans Vulval Davelopment.";

HO1. Cell 7:461-473(2001).

EMBL; AV028167; AAR19023.1;

HSSP; Q16254; LCF7

10terFro; IRR003316; E2F_TDP.
Pfam; PF02319; E2F_TDP; 1

SEQUENCE 287 AA; 32373 MM; 4344446E88F
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09FET1;
01-MAR-2001
01-MAR-2001
01-DEC-2001
DP PROTEIN.
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01-JUN-2001
01-DEC-2001
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"Characterization of wheat DP, a heterodimedization partner of the
plant EZF transcription factor which stimulates E2FIDNA binding.";
FEBS Latt. 486:73-78(2000).
EMBL: AJ271917: CAC19034.1;
EMBL: AJ271917: CAC19034.1;
INCEPT: Q14188: 12F07.
INCEPT: Q14188: 12F00316: E2F_TDP.
Pfam: PF00319: E2F_TDP; 1.
SEQUENCE 261 AA: 29262 NM; 5008DBF193163A28 CRC64;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; Pooldeae;
Triticeae; Triticum,
                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Bukaryota: Hetazos; Hematoda; Chromadoras; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
NEDLINE-21394624; PubMed-11463372;
Ceol C.J., Horvitz H.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (831B60
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                                                                                                                                                                                                                                                                                                 NCBI_TaxID-6239;
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KNIRRRYYDALNYFWALDIIARDKKEIRWKGLP 135
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1 (TrEMBLIEL 19,
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(TrEMBLIE).
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75.01;
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Pred.
  Score 82.5; DB 5; Pred. No. 0.0014;
                                                                            4344445E88E8C7A8 CRC64;
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ismatches 2;
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Best Local Similarity 50.4
Matches 17; Conservative
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                                                                              SEQUENCE FROM N.A.
TISSUE-TEMPORAL LOBE RIGHT;
OBAGA N., HIGH N., Kusuda J., Tenuma R.,
SIZUKI Y., Sugano S., Hashimoto K.?
"Isolation of full-length cDNA clones fr
libraries.";
Submitted (APR-2001) to the EMBL/GenBank
EMBL; AB060895; BAB46898.1; ".
                                                                                                                                                                                                                                        O95KG1 PRELIMINARY; PRT; 281 AA.

Q95KG1,
Q95KG1,
Q95KG1,
Q95KG1,
Q95KG1,
Q95KG1,
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 21, Last annotation update)
RPD/RHTICAL 31.7 KDA MOOTEIN.
Nacaca fascicularis (Cab sating macaque) (Cynomolyus monkey).
Nacaca fascicularis (Cab sating macaque) (Cynomolyus monkey).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Butheria: Primates; Catarrhini; Cercopithecidae;
Cercopithecinae: Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Bukaryota; Hetasoa; Nematoda; Chromadorga; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Investigating biology.*;
Science 383:3012-2018(1998).
Science 383:3012-2018(1998).
SMBL; ALL17303; CAS60421.1;
HSSP; Q10254; 1CF7.
HSSP; Q10254; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9U289
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NEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1999)
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                                          Hypothetical
SEQUENCE 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 RRRVYDALAVLAANNISK-EKREIKWIGLPTNS 36
:||||| :||| : | || |:||| ||
71 KRRVYDVINVLEGLGYVEKVEKNNIRWIGDNNNS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRRYTDVINVLEGLGYYDRYBKNNIRWIGDNNNS 107
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281 AA; 3
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                                                                                  EMBL/GenBank/DDBJ
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Pred, No. 0.0021;
5; Mismatches 11;
                                                                                                                                                                        Tanuma R., Iseki
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                                              PD71A9F7C2EEE0E5 CRC64;
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Query Match
Best Local Similarity 48.3%; Prec. No. 0.036;
Hatches 14; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
Oy 4 RRRYDALMYLMAMMISKE-KKEIKNIG 31
Db 100 KRRYDDITMYLDGIDLYEKRSKHIRNIG 128
Search completed: August 28, 2002, 13:03:00
Job time: 221 sec

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Title: Perfect score: Sequence:

US-09-900-147-1 186

OM protein -

Scoring table:

Maximum DB

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length: 0 length: 2000000000

Database :

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

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Post~processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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193.644 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen
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E2F-1 transcription
transcription fact
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protein 7286.2 (im
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Cranscription factor ORTF1 chain 1 - mouse
Cranscription in Subscription in Cranscription factors EZF-1 and DP-1 leads to Cranscraption Dev. 7, 1850-1861, 1993
A. Fills: Heterodimerization of the transcription factors EZF-1 and DP-1 leads to Cranscreamen Dev. 7, 1850-1861, 1993
A. Fills: Heterodimerization of the transcription factors EZF-1 and DP-1 leads to Cranscraption Dev. 7, 1850-1861, 1993
A. Fills: Heterodimerization of the transcription factors EZF-1 and DP-1 leads to Cranscraption Dev. 7, 1850-1861, 1993
A. Fills: Heterodimerization of the transcription factors EZF-1 and DP-1 leads to Cranscraption BRSS; MUID:94010284
A. Fills: Heterodimerization of the transcription factor Shown; not compared with conceptu A. Fills: Propries MRNA
A. Fills: Heterodimerization of the transcription factor Shown; not compared with conceptu A. Fills: Propries MRNA
A. Fills: P
RESULT 2
A48585

L'Engeription factor DP-1 - human
C'Species: Homo sapiens (man)
C'Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 10-Dec-1999
C'Accession: A48585
R;H011n, K.; HU, C'L.; Fattaey, A.R.; Lees, J.A.; Dynlacht, B.D.; Ngwu, C.; Harlow Genes Dev. 7, 1850-1861, 1993
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Best Local Similarity 100.01;
Matches 37; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
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7 Pred. No. 3.38-18;
0; Mismatches 0;
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TAB3991
G97111
G71510
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I69664
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Score

Match

Length 8

100.0 100.0 100.0 89.3 87.3 81.2

Caps

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A;Gene: GDB:TFDP2; DP2
A;Cross-references: GDB:638814
A;Map position: J923-3q23
A;Mare: DKF2p434G222.1
C;Superfamily: transcription factor DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Ansorge, N; Nirkner, U.; Meves, H.W.; Gassenhuber, J.; Wiemann, S. aubmitted to the Protein Sequence Database, June 1999
A;Reference number; 217527
A;Recession: 712511
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A;Status: preliainary; nucleic acid sequence not shown
A;Status: cype: mara
A;Residues: 1-410 <BEL>
A;Residues: 1-410 <BEL>
G;Stoss-references: GB:L23959; NID:g414316; PIDN:AAA58440.1; PID:g414317
C;Superfamily: Cranscription factor DP
C;Reywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K:Emang, Y.; Challappan, S.P.
Oncogene 10, 2083-2033, 1995
R:Title: Closing and characterization of human DP2, a novel %:Reference number: 137297; MUID:95303470
VAccession: I37797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Crose-references: EMBL:ALD80206
A;EXPERIMENTAL SOUTCE: adult testis; clone DKF2p434G222
R;Mu, C.L.; ZuNerberg, L.R.; Ngwu, C.; Harlow, E.; Lees, J.A.
R;Mul, Cell, Biol. 15, 2536-2546, 1995
Mol. Cell, Biol. 15, 2536-2546, 1995
M;Title: In vivo association of E2F and DF family proteins.
A;Reference number: A57381; MUID:95257935
A;Recession: A57381
                                                                                       Query Hatch
Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; translated from GB/EMBL/DDBJ: Molecule type: mRNA Residues: 'M', 33-49 <2HAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; translated from GB/EMBL/DDBJ Holecule type: mRNA
Residues: 'YP: mRNA
Cross-references: BMBL:U18422; NID:9604478; PIDN:AAB60378.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
Residues: 'M',33-416 <MUA>
CTOSE-TETETENCES: CB:L40386; NID:9703084; PIDN:ANA69016.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Homo sapiens (man)
Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 17-Nov-2000
Accession: T12511: A57381: 137297: 139180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: SMBL: U35117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 KNIRRKYTDALHYLMAMNIISKEKKEIKWIGLPTNSA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KNIRRRYTDALNYLMANNIISKEKKEIKWIGLPTNSA 3:
1 KNIRRRYZDALMYLMAMHIISKEKREIKWIGLDTNSA 37
                                                                                       37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-416 <ANS>
                                                                                       Conservative
                                                                             100.0%; Score 186; DB 2: Length 416; 100.0%; Pred. No. 5.4e-18; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 186; DB 2;
100.0%; Pred, No. 5.3e-18;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                  NID:g1008545; PIDN:AAC50642.1; PID:g1008546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E2F-1 and DP-1 leads to coopera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dimerization partner of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:9703085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:9604479
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                                                                                Caps
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                                                                                0
                             hypothetical protein T23G7.1 - Caenorhabditis elegans C:Species: Ceenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t/ C:Accession T252O7 R:Barlov, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Genetics:
A;Gene: PlyBase:Dp
A;Gene: references: FlyBase:FBgn0011763
A;Cross-references: PlyBase:FBgn0011763
C;Superfamily: transcription factor DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factor DRFF1 chain 1 - mouse
N;Alternate names: transcription factor DP-1
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Dec-1999
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Dec-1999
C;Accession: $30049; $34572
R;GIT11ng, R: Partridge, J.F.; Banders, L.R.; Burden, N.; Totty, N.F.; Hauan, J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type; protein
A; Residues: 75-90; 111-131; 164-184; 191-207; 235-249; 281-293; 302-313; 321-328 <GJR2>
C; Superfently: transcription factor DP
C; Reywords: DNA binding; transcription factor
F; 84-204/Domain: DNA binding #status predicted <DNA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: A new component of the transcription factor DRTP1/E2F A; Reference number: $30049; MUID:93188967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Dynlacht, B.D.; Brook, A.; Dembski, M.; Yenush, L.; Dyson, M. Proc. Natl. Acad. Sci. U.S.A. 91, 6359-6363, 1994
A;Title: DNA-binding and trans-activation properties of Drosophila A;Reference number: A55745; MUID:94294381
A;Accession: B55745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription factor DP - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Araccession: 834572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross·references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-429 <GIRl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S30049
submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 89.2
Best Local Similarity 86.1
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Drosophila melanogaster
Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 186: DB 2: Best Local Similarity 100.0%; Pred. No. 5.60-18; Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: BS5745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KNIRRRYTDALNYLJAMNIISKEKKEIKNIGLPTNSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 KNIRRRYDALNYLWAMNIISKEKKEIKWIGLPTNSA 184
                                                                                                                                                                                                                                                                                     145 KNIRRRYDALNYLMAINVISKDKKEIRWIGLPANS 180
                                                                                                                                                                                                                                                                                                                  1 KNIRRRYKDALNYLMAMNIISKEKKEIKHIGLETNS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: X72310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB: X79708; NID: g516866;
                                                                                                                                                                                                                                                                                                                                                                                                                         89.24;
                                                                                                                                                                                                                                                                                                                                                                                               Score 166; DB 2;
pred. No. 2.9e-15;
4; Mismatches 1
                                                                                15-Oct-1999 #text_change 15-Oct-1999
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Length 429;

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10-Dec-1999

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A; Nap position: 5
A; Introns: 84/2; 1
A; Note: 91224.160
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A;Molecule type: DAA
A;Molecule type: DAA
A;Rosidens: 1-598 CMIL>
A;Cross-references: EMBL:268319; PIDN:CAA92699.1; GSPDB:GN00020; CESP:72367.1
A;Experimental source: clone T2367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription factor-like protein - Arabidopsis chaliana N;Alternate names: protein F1264.160 C;Speciaes: Arabidopsis chaliana (mouse-ear creas) C;Speciaes: Arabidopsis chaliana (mouse-ear creas) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: 748364 R;Bevan, M.; Pohl, T.; Welzenegger, T.; Bancroft, I.; Mewes, H.N.; Rudd, S.; Submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: 219995
A; Accession: 725207
                          A; Map position: 5
A; Introns: 36/2; 1
                                                                                                 A.Status: preliminary
A.Molecule type: DA
A.Molecule: 1-288 GEV>
A.Cross-references: EMBL:AL162971
A.Experimental source: cultivar Columbia: BAC clone T22P11
                                                                                                                                                                                                                                                                                                                                                                                                                 DP-2 transcription factor-like - Arabidopsis thaliana N; Alternate names: protein 122011.60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Molecule type: DNA
;Residues: 1-413 (ERV)
;Cross rafarences: ENB:;AL162731
;Experimental source: cultivar Columbia: BAC clone F12E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 81.20;
Best Local Similarity 83.30;
Matches 30; Conservative 3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                   Reference number: 124490
Accession: 748268
                                                                                                                                                                                                                                                                                  Species: Arabidopsis thaliana (mouse-ear cress)
Oste: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
Accession: 748268
Beyan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.;
bmitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 avan, M.; Pohl, T.; Metenegger, T.; Bancroft, T.; Mewes, H.N.; Rudd, S.; Lencke,
Mitted to the Protein Sequence Database, March 2000
Merence number: 124492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T22P11.60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                    57/1; 71/3; 95/3; 142/3; 169/3; 198/3; 222/2
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Pred. No. 3.2e-13;
7; Mismarches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 151; DB 2; Length 413; Pred. No. 4e-13; 3; Mismatches 3; Indels
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equal
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RESULT 11 A56209

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C; Species: Mus musculus (house mouse)

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C;Genetics:
A;Gene: CESP;Y48C3A.t
A;Introns: 93/3; 156/2; 206/2; 237/3; 332/1; 386/1
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C;Species: Caenorhabditis elegans
C;bate: 29-Oct.1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 734C20.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 13-Aug-1999 ssequence_revision 13-Aug-1999 stext_change 22-Oct-1999
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A;Molecule type: DNA
A;Regiduss: 1-470 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Wallis, J.
submitted to the EMBL Data Library, September 1999
A; Reference number: Z21046
A; Accession: T31602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Reference number: 217586
A:Accession: T13005
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A;Experimental source: clone Y48CJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSAVII.

MACCESSAVII.

MACCESSAVII.

MACCESSAVII.

MACCESSAVIII.

MACCESSAVII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, e Protein Sequence Database, July 1999
                                                                                                                                                                                                                                                                                                                                     , 29/3; 55/3; 73/3; 111/1; 139/3; 159/1; 179/3
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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75.6%;
                                                                                                                                                                                               38.7%;
                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                   Score 72; DB 2;
Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 136;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nismatches
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                                                                                                                                                                8
                                                                                                                                                                                                                                       Length 323;
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A:Cross-references: GB:H96577; NID:g181917; PIDM:AAA3782.1; PID:g181918
A:Cross-references: GB:H96577; NID:g181917; PIDM:AAA3782.1; PID:g181918
A:Experimental source; Naim 6 pre-B Laukemia cell line
A:Exte: sequence extracted from NCBI backbone (NCBIN:110015, NCBIP:110016)
R:Kaelin Jr., N.G.; Krek, N.; Sellers, N.R.; DeCaprio, J.A.; Ajchenbaum, P.; Fuchs, C Cell 70, 351-364, 1992
A:71tle: Expression cloning of a cDNA encoding a retinoblastoma-binding protein vith A.R.ccession: A42997; NVID:92346721
A.R.ccession: A42997; NVID:92346721
A.R.ccession: A42997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription factor E2P1 - human

**Alternate names: Ap12 protein; retinoblastoma-associated protein; retinoblastoma-bindi
C:Species: (Name Sapiens (man)
C:Date: 22-Oct-1996 *sequence_revision 01-Nov-1996 *text_change 02-Jun-2000
C:Accession: JC4929; A45032; A42998; A42997; I54091
R:Neuman, E; Sellers, W.R.; McNeil, J.A.; Lavrence, J.B.; Kaelin Jr., W.G.
Gene 173, 163-169, 1996
A:Title: Structure and partial genomic sequence of the human E2F1 gene
A; Rccession: JC4929; MUID:97082961
A; Accession: JC4929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Experimental source: placenta R;Shan, B:; Zhu, X.; Chen, P.L.; Durfee, T.; Yang, Y.; Sharp, D.; Lee, W.H. R;Shan, B: Zhu, X.; Chen, P.L.; Durfee, T.; Yang, Y.; Sharp, D.; Lee, W.H. Mol. Cell. Biol. 12, 5620-5631, 1992

A;Title: Molecular cloning of cellular genes encoding retinoblastoma-associated A:Reference number: A45032; MUID:93078763

A:Recession: A45032; MUID:93078763
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                                        A; Wolecule type mRNA.
A; Residues: 1:312,'S',314-321,'M',323-328,'T',330-437 <KAES
A; Residues: 1:312,'S',314-321,'M',323-328,'T',330-437 <KAES
A; Ricoes: references: GB:U13851; NID:g555713
A; Experimental source: Akata cells: axpression vector pGEX-27K
A; Natce: sequence extracted from NCB backbone (NCBIN:110018, NC
R; Johnson, D.G.; Ohtani, K.; Nevins, J.R.
Genes Dev. B, 1514-1525, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Holecule type: mRNA
A:Realduss: 'LCRORRPOAERDRALAEACRHGDAPPPPPPVTRAARAVSV',1-312,'S',314-321,'N',323-328,'T',
A:Realduss: 'LCRORRPOAERDRALAEACRHGDAPPPPPPVTRAARAVSV',1-312,'S',314-321,'N',323-328,'T',
A:ROCE: sequence extracted from NCBI backbone (NCBIE:119095)
A:NOCE: the authors are uncertain whether Het-1 is the initiator or whether translation
R:Hello, X.; Lees, JA.; Vidal, M.; Dyson, N.; Harlow E.; Fattaey, A.
Cell 70, 337-350, 1992
A:Title: A cDNA encoding a pRB-binding protein with properties of the transcription fact
A:Reference number: A42998; MUID:93346720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Status: preliminary: nucleic acid sequence not shown
A:Holecule type: DMA
A:Residues: 1-137 (ANGU)
A:Rossidues: 1-137 (ANGU)
A:Rossidues: 1-137 (ANGU)
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A;Title: Cloning, Chromosomal location, and characterization of mouse E2F1.
A:Reference number: A56209; MUID:94158858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:L21973; NID:g1091479; PIDN:AAAB3217.1; PID:g405524
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Accession: A56209
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Residues: 1-430 <LIA>
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Ory control of E2F1 expression 154091; MUID:95047311
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                             response
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                             positive and
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                                                                                                                                                                                                                                                                                                                                                 82
                                                       A; Map position: 1p36-1p36
C; Keywords: transcription
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AS4595
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A;Cross-references: EMBL:X89245; NID:g944827; PID:g944828
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A)Cross-references: GDB:134661; OMIM:189971
A;Mdp position: 20011-2011
A)Interons: 87/3 118/1 191/2 242/2 280/3 356/1
C;Reywords: DNA binding: transcription factor 5:67-2108/Region: cyclin box Status predicted F:118-190/Domain: DNA binding status predicted
                                                                                                                                                                                                                   F; 191-241/Region:
                                                                                                                                                                                                                                                                                                                                                                              ;Accession: 154091
;Status: preliminary: translated from GB/EMBL/UUDD
;Holecule type: DNA
;Residues: 1-88,'R','T',122-123,'TPR',127,'QRR',297-299,'PRR',308-309,'RA',312,'C'
;From references: GB:S74230; MID:g712816; FIDM:AAD14150.1; FID:g4261850
                                                                                                                     Query Match 38.41;
Best Local Similarity 43.8%;
164 KRRIYDITNVLEGIQCIAKXSKNHIQMLGSHT 195
                                                  4 RRRVYDALHVLMAMNIISKE-KKEIKWIGLPT 34
                                                                                                   Conservative
                                                                                                                                                                                                                      7-residue
                                                                                                8; Mismatches
                                                                                                                        Score 71.5; DB Pred. No. 0.05;
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                                                                                                   9
                                                                                                                                                Length 437;
                                                                                                   Indels
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A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-403 <PAS> R;Pastesu, S.; Loisesu, L.; Arnaud, L.; Trembleau, A.; Brun, G. submitted to the EMRL Data Library, June 1993
A;Description: Isolation and characterization of a chicken homolog A;Reference number: \$58345
A;Accession: \$58345 IP-1 transcription factor - chicken
;Species: Gallus gallus (chicken)
;Sate: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 10-Sep-1991 Accession: 558345 of the E2P-1 tre

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R:Ivey-Hoyle, M.; Conroy, R.; Huber, H.E.; Goodhart, P.J.; Oliff, A.; Heimbrook, Mol. Cell. Biol. 13, 7802-7812, 1993
A;Title: Cloning and characterization of EZF-2, a novel protein with the blochemia; Reference number: A54595; MUID:94067141
A;Recession: A44595
A;Recule type: mRNA
A;Residues: 1-437 (IVE)
                                                                                                                                                                                                                                                                                                 A/Cross-references: GDB:270248; OMIM:600426
A:Hap position: 1p36-1p36
                                                A; Gene: GDB:E2F2; E2F-2
                                                                                             A;Cross-references: GB:L22846; NID:g410206; PIDN:AAA16890.1; PID:g410207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.9%;
Best Local Similarity 44.8%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * RRRYYDALNYLMAMNIISKE-KKEIKWIG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70.5; DB 2; Length 403;
Pred. No. 0.063;
B; Mismatches 7; Indels
                                                                                                                                                                                                                                 protein with the blochemics
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-805 <00H7>
A;Residues: 1-805 <00H7>
A;Residues: 1-805 <00H7>
A;Cross-references: GB:Ul0184; NID:g499103; PIDN:AAA19003.1; PID:g499104
A;Cross-references: GB:Ul0184; NID:g499103; PIDN:AAA19003.1; PID:g499104
R;Dynlacht, B.D.; Brook, A.; Dembskl, K.; Yenush, L.; Dyson, N.
Proc. Natl. Acad. Sci. U.S.A. 91, 6359-6363, 1994
A;Title: DNA-binding and trans-activation properties of Drosophila E2F and DP proteins.
A;Reference number: A55745; MUID:94294381
A;Accession: A55745
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G;Spacies: Drosophila melanogaster
G;Date: 28-Apr-1995 sequence_revision 28-Apr-1995 stext_change 21-Jul-2000
G;Accession: A56199; A55745
R;Ohtani, K.; Nevins, J.R.
Mol. Cell. Biol. 14, 1603-1612, 1994
Mol. Cell. Biol. 14, 1603-1612, 1994
A;Title: Functional properties of a Drosophila hcmolog of the E2F1 gene.
A;Reference number: A56199; MUID:94158833
A;Accession: A56199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: PlyBase:E3f1
A;Cross-references: FlyBase:FBgn0011767
       Search completed: August 28, 2002, 12:59:59 Job time: 130 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Overy Match 36.3%; Score 67.5; DB 2; Length 805; Best Local Similarity 48.1%; Pred, No. 0.36; Matches 13; Conservative 6; Mismatches 7; Indels
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291 KRRIYDIYHYLEGINILEKKSKNNIGH 317
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j.
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GenCore version 4.5
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Run on:
                                                                                                              OM protein - protein search, using aw model
August 28, 2002, 12:55:14; Search time 29.9 Seconds (without alignments)
137.449 Million cell updates/sec
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Title: Perfect score: Sequence: US-09-900-147-1 186

1 KNIRRRYYDALNYLMAMNIISKEKKEIKWIGLPTNSA 37

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 segs, 111073796 residues

Searched:

fotal number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match (%)
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_03802:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1981.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1981.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1981.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1981.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1981.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1985.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1985.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1985.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1988.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1988.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1989.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1989.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1990.DAT:* | SIDS1/gcgdate/hold-geneseq/geneseqp-emb1/AA1990.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by enalysis of the total score distribution.

SUMMARIES

| • | 70 |
|--|----------------|
| 11 1000/64**** | Result |
| 1562 1562 1563 1563 1566 1566 1566 1566 1566 1566 | Score |
| 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 | Query Match |
| 1184424 | Length |
| 222222222 | 80 |
| AAW30501 ABG05510 AAG74072 AAR54663 AAR89212 ABR28057 AAY18026 ABB60892 ABB60892 ABB60893 ABB33108 AAB33109 | מו |
| DP-1 transcription Novel human diagno Human colon cancer Transcription fact Transcription fact Novel human diagno Murine DP-Jalpha 1 Drosophila melanog Novel human diagno Pinus radiata tran Pinus radiata tran | Description |

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AAW30501 standard; Peptide; 37 3

AAW30501;

26-OCT-1998 (first entry)

DP-1 transcription factor paptide H (DEF box).

DP-1; transcription factor; antagonist; E2P protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.

Synthetic. Homo sepiens.

W09828334-A1.

02-JUL-1998.

22-DEC-1997; 97WO-GB03506

20-DEC-1996; 96GB-0026589

(PROL-) PROLIFIX LTD.

Bandara LR. La Thangue NB;

WPI: 1998-377596/32.

Polypeptide fragments of the DP-1 transcription factor \cdot used for inducing apoptosis, specifically in tumour and cardiovascular cells. e.g. for preventing restanosis

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Peptide # (I) comprises residues 163-199, i.e. the DEF box region, confirmation of transcription factor DP1. Claimed fragrants (II) (see AN#30502-07) CC of (I) are capable of antagonising the heterodimentation of a DP cc of (II) comprising (I) or (II) and a membrane translocation sequence (III) comprising (I) or (II) and a membrane translocation sequence (CC (II)-(III) are used therapeutically to induce apoptosis, cells. (CC (I)-(III) are used therapeutically to induce apoptosis, comprising thro, e.g. for purging bone marrow. Surgical stents comprising vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating compact of DP/E2F heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-/Z2F dimerisation and as immunoassay (I)-(III) to control DP levels in cells, particularly by gene therapy. When formulated with cytotoxic cor cytostatic agents, (I)-(III) enhance cell killing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 37
New isolated polynucleotide and encoded polypaptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                         N-PSDB; AAS69697.
                                                                                                                                                                                                                        Drmanac RT.
                                                                                                                                                                                                                                                                             (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #5501.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 100.0%; Score 186; DB 19;
Local Similarity 100.0%; Pred. No. 9.8e-22;
hes 37; Conservative 0; Mismatches 0;
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                                                                                                                                                                  2001-639362/73.
                                                                                                                                                                                                                                                                             HYSEO INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 A.;
                                                                                                                                                                                                                    Liu C,
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Claim 20; SEQ ID No 35869; 103pp; English.

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer easociated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene

invention relates to isolated polynucleotide (I) and

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cc polypeptide (II) sequences. (I) is useful as hybridisation probes, co polymerase chain rescrion (PCR) primars, oligomars, and for chromosome cc and gene mapping, and in recombinant production of (II). The crimens of the polymerase chain recombinant production of (II). The crimens of the polymerase are also used in diagnostics as expressed sequence tags of crimens of the polymerase are also used in diagnostics as expressed sequence tags of (II). (II) is useful for generating antibodies against it, detecting or (II), (II) is useful for generating antibodies against it, detecting or a food supplement, (II) and its binding partners are useful in medical considers and sequence supplement, (II) and its binding partners are useful in medical considers involving aberrant protein expression or biological activity. Crimany of sites expressing (II). (I) and (II) are useful for treating crimany of the polypeptide and polymicleotide sequences have applications in the polypeptide and polymicleotide sequences have applications in the produce other types of data and products dependent on DNA and and content of the produce other types of data and products dependent on DNA and the product sequences. ABG10010-ABG10017 represent novel human crime in the sequence data for this patent did not appear in the printed at for this patent did not appear in the printed of the time in the printed at for this patent did not appear in the printed of the time in the printed at for this patent did not appear in the printed at for this patent did not appear in the printed at for this patent did not appear in the printed at for this patent did not appear in the printed at for this patent did not appear in the printed at for this patent did not appear in the printed at for this patent did not appear in the printed at for this patent did not appear in the printed at for this patent did not appear in the printed at for the patent did not appear in the printed at for the patent did not appear in the printed at for the patent did not appear in the 
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Best Local Similarity 100.0%;
Matches 37; Conservative 0
                                                                                                                  Claim 11;
                                                                                                                                                        Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                            WPI; 2001-235357/24.
N-PSDB; AAH33503.
                                                                                                                                                                                                                                                                                          Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinome; chromosome 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human colon cancer antigen protein SEQ ID NO:4836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                            Page 6620-6621; 9803pp; English.
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9908-0163780.
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Pred. No. 5.3e-21;
), Mismatches 0;
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RESULT
AAR54663
ID AAR5
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Best Local Similarity 100.0%;
Matches 37; Conservative 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat discrease associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing insetive proteins or to supplement the patients own production of P. additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the color cacers. The protesins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAH37789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR54663;
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DNA encoding novel transcription factor DP-1 was obtained from P9-EC cells. The DNA can be used to produce recombinant DP-1, or in gene therapy as a means of treating the uncontrolled proliferation of a.g. tumor cells.
                                                                                                                                                                                 Novel transcription factor DP-1 and its recombinant production . for diagnosis end treatment of diseases associated with abnormal ETF or ETF-1 and family expression, esp. proliferative diseases
                                                                                                                                                                                                                                                                                                WPI; 1994-167464/20.
N-PSDB; AAQ65344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-1992;
05-AUG-1993;
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N.B. Pages 666 to 682 and page 7053 of the sequence listing were
missing at time of publication, meaning no sequences are present for
SBQ ID ND:1037 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                 LA THANGUE NB;
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                                                                                                                                    Disclosure: Page 49-50; 74pp; English.
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93GB-0016206.
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Pred. No. 1.5e-20;
Hismatches 0;
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SACCCCCASAPPPADDAPAPAPAPAPAPA

Sequence

410 AA;

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Ouery Match 100.0%; Best Local Similarity 100.0%; Matches 37; Conservative 0;

Score 186; DB 17; Pred. No. 1.8e-20; ; Mismatches 0;

Length

10;

Indels

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Best Local Similarity
Matches 37; Conserv
                  DP-1 (ANRB9212) is part of the DP-1/E2P-1 transcription factor complex. It is phospharylated during the cell cycle, and has a greater affinity for IMB when in a hypophosphorylated state. This finding can be used to 4ssay for agents which prevent or inhibit DP-1 hypophosphorylation or which enhance the phosphorylation of DP proteins. Such agents can be used to prevent or delay entry of the cell cycle into 5 phase from G1 useful in tranting proliferative diseases. Antibodies against regions of DP-1 which undergo changes in phosphorylation (see AAR8913) can also be used in such assays, and to identify proliferating cells.
                                                                                                                                                                                Assays for potential growth prevention, inhibiting or enhancing agents - asp. DP protein phosphorplation modulation agents, used to provent or delay entry of cell into S phase from G, useful in treating proliferative diseases
                                                                                                                                                                                                                                                                                                                                                             03-JUL-1995;
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phosphorylation; cell proliferation; therapy; diagnosis.
                                                                                                                                                            Claim 6: Page 38-40; 54pp; English
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                                                                                                                                                                                                                                                                                                             (MEDI-) MEDICAL
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DB; AAT10582.
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ilarity 100.0%;
Conservative 0
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Pred. No. 1.8e-20;
Nismatches 0;
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CC the invention relates to isolated polynucleotide (I) and CC polymeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerse chair reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II) are continued for interested genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful in gene therapy techniques CC (II). (II) is useful in gene therapy techniques CC (II). (II) as so noiseular veight askers and as a food supplement. (II) and its binding partners are useful in medical CC inaging of sites expressing (II). (I) and (II) are useful for treating CC inaging of sites expressing (II). (I) and (II) are polymentical contractions in CC inaging of sites expressing (II). (I) and (II) are polymentical correlates, gene mapping, identification of mutations in CC dispositios in polymerical disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and CC aniso acid sequences as AscQ0010-AsQ3017 represent novel human CC aniso acid sequences dependent on contact appear in the printed CC specification, but was obtained in electronic format directly from WIPO at first two polymers of the invention.
                                                                Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polyneptides, useful in disgnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 58416; 103pp; English.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
N-PSDB; AAS92244.
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Homo sapiens
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                                                                                                                                           424 AA:
                                                           Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                                           Score 186; DB 22;
Pred. No. 1.9e-20;
); Mismatches 0;
                                                                                          Length 424;
                                                              Indels
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                                                             Gaps
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RESULT
NAY18026
ID ANY1
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CC The invention relates to the DP-Interacting protein (DIP), that contains the invention relates to the DP-Interacting protein (DIP), that contains the BIP-POP. domain, and is a potent transcriptional repressor that can call and immunogen or to raise antibodies. Such antibodies are useful in the purification and disgnostic screening methods. DIP polypeptides may be used to screen for modulate its activity. Such molecules used to serve for modulate its activity. Such molecules are useful in therapeutic contexts, e.g. in connection with conditions thick involve abnormal or abstrant expression of DIP. Modulators of DIP completed to promote cell cycle control or modification in conditions and be used to promote cell cycle control or modification in conditions are useful as sources of probes and primers, and for collectides are useful as sources of probes and primers, and for conditions associated with disorders of surents, variants and conditions associated with disorders of germ cells, including proliferative disorders such as deminomas and teratomas.
                                                                                                                                                                                                                                                                  Query Match 97.8%;
Best Local Similarity 97.3%;
Matches 36; Conservative
ABB60852 standard; Protein; 445
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De La Luna S, La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIP: DP-interacting protein; BTB/POZ domain; transcriptional repressor; DP-dependent transcription; immunogen; cycle control; seminome; teratome diagnosis; meiosis promoter; proliferative disorder; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY18026 standard; Protein; 446
                                                                                                                                           Dischosure; Page 73-76; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DP transcription factor-interacting protein designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-347716/29.
N-PSDB; AAX76730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Н09927091-А1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nurine DP-3alpha isoform protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIU ) UNIV GLASCOW.
                                                                                                                                                                                                                                                                                                                                                                                                                           116 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97GB-0024828
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                                                                                                                                                                                                                                                                                              Score 182; DB 20;
Pred. No. 8.4e-20;
                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                             Length 446;
                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                     Caps
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26-MAR-2002 (first entry)

ABB60852;

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

Drosophila melanogaster polypeptide SEQ ID NO 9348.

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                                                                                                                                                                                                                                                                                                                               Ouery Match 89.2%;
Best Local Similarity 86.1%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more games from Drasophila. The invention useful in developmental biology and in elucidating cell signaling and cell-cell interactions in higher sukaryotes for the development of insecticides, therapautics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL51616-ABL51615-ABL511), expressed DNA sequences (ABL51819-ABL7072).

(ABB77072).

(ABB77072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. Mipo.int/pub/published_pct_sequences.
30-MAR-2001; 2001WO-US08631.
                           11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 9348; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI: 2001-656860/75.
N-PSDB; ABL04955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000U8-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001NO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W0200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                   W0200175067-A2
                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                    Novel human diagnostic protein #5499.
                                                                                                                                                              13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY
                                                                                                                                                                                                                ABG05508 standard; Protein; 185
                                                                                                                                                                                                                                                                           445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'ama 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                           Score 166; DB 22;
Pred. No. 2.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Муег 9
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                                                                                                                                                                                                                                                                                                                                                        Length 445;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                               Gaps
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The invention relates to isolated polynucleotide (I) and CC polyspeptide (II) sequences. (I) is useful as hybridisation probes, polyspeptide (II) sequences. (I) is useful as hybridisation probes, polynucleotides are also used in disgnostics as expressed sequence tags of polynucleotides are also used in disgnostics as expressed sequence tags (I) is useful in gene therapy techniques (I) is useful in gene therapy techniques (II). (II) and its binding apriners it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical companies in the sequences in a sequence have applications in the polypeptide and polymucleotide sequences have applications in CC disgnostics for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC and ocid sequences a ABG00010-ABG10377 represent novel human CC disgnostic mino acid sequences of the invention.

CC disgnostic mino acid sequences of the invention of the printed companies of the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 35867; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleptide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000;
23-AUG-2000;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Llu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-639362/73.
DB; AAS69695.
   185 AA;
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2000US-0649167.
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                              Query Match
Best Local Similarity
Matches 33; Conserv
milarity 89.2%;
Conservative
                              Score 162; DB 22;
Pred. No. 3.8e-17;
2; Mismatches 2;
                                               Length 185;
                                 Indels
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RESULT 10
AAB33108
ID AAB3311
XX AAB3311
XX 25-JAN
XX 25-JAN
XX Plant;
XX Plant;
XX Poplat
XX Poplat
XX Poplat
XX Poplat
XX Poplat
XX Vype 2
OS Pinus
XX Vype 2
OS Pinus
XX W02000
XX W02000
XX W02000
                                                                                                                 Plant; transcription factor; gene expression; eucalyptus; pine; acacla; poplar; sweetgum; teak; mahogang; bill; G-box binding factor; basic halix-loop-helix zipper; homeotic; homeodomain; homeobox; WADS; homeodomain zipper; LIM domain; AP3; EREBs; zinc linger domain; type 2 Cys3His3; CCANT box element; MYB.
                                                                                                                                                                                                                                                                                                                                                  AAB33108 standard; Profile; 119 AA
                                          NO200053724 - A2
                                                                              Pinus radiaca.
                                                                                                                                                                                                                                   Pinus radiata transcription factor protein sequence #235.
                                                                                                                                                                                                                                                                           25-JAN-2001 (first entry)
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Best Local Similarity 86.1
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiate. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a sucalyptus, plane, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polyperide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: b2IP, b2IP family of G-box binding factors, basic helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain inper, lim domain, AP2 and BREBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements and MYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant: transcription factor; gene expression; eucalyptus; pine; acacla; popilar; sweetgum; tesk; mahogan; bire; G-box binding factor; basic helix-loop-helix ripper; homeotic; homeodomain; homeobox; WADS; homeodomain ripper; LIN domain; AP2; EREBs; rinc finger domain; type 2 Cys2His2; CCAAT box element; MYB.
                                                                                                                      11-MAR-1999;
18-AUG-1999;
                                                                                                                                                                                                                                        09-MAR-2000; 2000WO-US06112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pinus radiata transcription factor protein sequence #134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB33007 standard; Protein; 120
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(GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD
                                                                                                                                                                                                                                                                                                                       14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                      WO200053724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pinus radiata.
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                                                                                                                 99US-0266513.
99US-0149485.
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990S-0149485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 158; DB 21;
Pred. No. 9.4e-17;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glenn H;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
                                  Novel LIN-37, -35, -55, -52, -53 and -54 gene from C. elegans - usaful for treating diseases associated with altered levels of cell proliferation, e.g. carcinomas
                                                                                             WPI, 19
                                                                                                                                      1093
                                                                                                                                                                                                                                                                                                                                LIN-55; synthetic multivulva; SynMuv; signal transduction; animal model; tumour suppressor; retinoblastoma; cancer; cancer; cell proliferation; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to novel plant transcription factors from Bugalyptus grandle or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a sucallyptus, pine, acacia, poplar, sweetgum, teak, or machogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bzIP, bzIP family of G-box binding factors, besic helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain in the proteins and BREBB, zinc finger domains of type 2 Cyszkisz, CCAAT box elements and MYB.
                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans synNuv protein LIN-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW83389 Standard; Protein; 575
                                                                                                                                                                                              28-MAY-1997;
                                                                                                                                                                                                                         28-MAY-1998;
                                                                                                                                                                                                                                                     03-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-579369/54.
                                                                                                                                                                 (NASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                MO9854299-A1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-045352/04
DB: AAV72852
                                                                                                                                     C, HOTVILZ HR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M, McGrath A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 83.:
30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 AA;
                                                                                                                                                                                                                     98WO-US11043.
                                                                                                                                                                                            9705-0047996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.31;
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Pred. No. 5.7e-16;
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Claim 7; Fig 8; 70pp; English

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RESULT 13
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Best Local Similarity 75.7%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP-1: transcription factor; antagonist; E2F protein; cell proliferation; cardiovascular cell; restenosis;
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WPI; 1998-377596/32.
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                                                   Bandera LR,
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5..15
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Pred. No. 3.8e-15;
7; Mismatches 2;
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Peptide H7 comprises amino acid residues 170-199 in the DEF box (II) (see AAN9501) of transcription factor DP1. Claimed peptides (II) (see AAN9504-07) containing one or both of 2 motife (see AAN9502-03) of the DEF box are capable of sntagonising the haterodimerisation of a by protein with an ZEP protein. Also claimed are verients of these peptides, especially containing substitutions of residues corresponding to residues 167, 159, 171 and 175 of DP-1, fusion proteins (II) comprising (I) or (II) and a membrane translocation sequence (see AAN9508), expression vectors encoding (I)-(III) and host cells. (I)-(III) are used to rerapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging the marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restencis in patients who have undergone to ansignisty of DP/EZF heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-1/EZF dimerisation and as immunoassay agents. Also described is the use of sequences on the natient about or cuttainly by gene therapy. When formulated with cytopoxic or cytostatic agents, and cell in a shape in cells, particularly by gene therapy. When formulated with cytopoxic or cytostatic agents.
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용 ð Query Match 81.7%; Score 152; DB 19; Best Local Similarity 100.0%; Pred. No. 1.5e-16; Matches 30; Conservative 0; Mismatches 0; Length 30; Indels 0 Caps

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Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells.

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9903-0121805
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25-FEB-2000; .2000EP-0301439

-APR-1999; -APR-1999; -APR-1999; -APR-1999;

| PR 20-7UL-1999 99US-0144613 PR 21-7UL-1999 99US-0144614 PR 21-7UL-1999 99US-0145085 PR 21-7UL-1999 99US-0145085 PR 22-7UL-1999 99US-0145085 PR 22-7UL-1999 99US-0145085 PR 22-7UL-1999 99US-0145181 PR 22-7UL-1999 99US-0146181 PR 22-7UL-1999 99US-0147181 PR 22-7UL-1999 99US-0148171 PR 22-7UL-1999 99US-0148181 PR 22-7UL-1999 99US-0155181 PR | | | |
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18-0C7-1
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Transgenic plants comprising an expression cassette consisting of a DP nucleic acid, when expressed, the nucleic acid increases the efficiency of plant cell transformation by increasing the number of dividing cells in the plant.
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                                                                                                                                                                                                                                                                                                                                          Zea mays.
                                                                                                                                                                                                                                                                                                                                                                  DP polypeptide: transcription factor; gene transcription; cell cycle; DNA replication; DRTF; differentiation-regulated transcription factor 1; transfermation efficiency.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB07975 standard; Protein; 299
                                                                      WPI; 2000-524530/47.
N-PSDB; AAA59702.
                                                                                                                                                                                             11-PEB-2000; 2000WO-US03651.
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                                                                                                                                        (PION-) PIONEER HI-BRED INT INC.
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Pred. No. 3,2e-15;
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Disclosure: Page 71-72: 76pp; English.

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                                         The present sequence represents a corn DP (not defined) polypeptide. The polypeptide is a transcription factor that activates transcription of numerous genes involved in DNA replication, thus playing a role in the G1 to S transition in the cell cycle. Do, also called DRTP (differentiation-regulated transcription factor 1) has been shown to form specific multiprotein complexes with the retinohastoms susceptibility protein, pl07, cyclins and cdk1. The DP polynucleotide proteins are useful for increasing transformation efficiency in plants by increasing the number of dividing cells in the plant (dividing cells may be more receptive to transformation).
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Sequence 299 AA;

Query.Match 81.2%; Best Local Similarity 83.3%; Matches 30; Conservative Score 151; DB 21; Pred. No. 3.5e-15; 3; Mismatches 3; Length 299; Indels 0 Caps

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Search completed: August 28, 2002, 12:59:14 Job time: 240 sec

Title: Parfact acore: Sequence:

US-09-900-147-1 186 1 RNIRRRVYDALAVU

RNIRRRYDALNYLMANNIISKEKKEIKWIGLPINSA

protein - protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugan

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. August 28, 2002, 12:59:34; Search time 10.33 Seconds (without alignments) 138.686 Million cell updates/sec Ol4186 homo sapien Ol6189 mus musculu Ol4188 homo sapien O24318 drosophila O24318 drosophila O24318 drosophila O24318 drosophila O54317 mus musculu O54317 mus musculu O54317 mus musculu O54317 mus musculu O75461 homo sapien O61501 mus musculu O10716 homo sapien O5937 gallus gall O4209 homo sapien O5361 rattus norv O51562 mus musculu O15363 homo sapien O25364 rattus norv O51563 mus musculu D53163 homo sapien O16264 rattus norv O16072 achizosach O50164 mus musculu O51072 achizosach O50172 achizosach O50172 achizosach O50172 schizosach O50173 mus musculu O50174 musculu O50176 mus musculu PI_HUMAN TDPI_HUMAN STANDARD; PRT; 410 AA. 014186; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-OCT-2001 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Transcription factor DP-1 (R2P dimerization part PO-1/POPICIO-1) (DRTP1). TFDP1 OR DP1 (DRTP1) HOMO Sapiens (Human). Eukaryotes Hetasca; Chordata; Craniata; Vertebra Mammalia; Eutheria; Primates; Catarrhini; Homini NCB1_TaxID-9606; [1] CHARACTERIZATION. HEDLINE-95257935; PubHed-7739937; Mu C.-L. Zukerberg L.R., Ngwu C., Harlow E., Lees J.A.; "In vivo association of E2P and DP family proteins."; hol. Cell. Biol. 15:3536-2546(1995). SEQUENCE FROM M.A., AND CHARACTERIZATION. HEDLINE-94010284; PubMed-9405999; Helln K., Wu C.-L., Pattagy A.R., Lees J.A., Dynlacht B.D., Mynu C., Harlow E.; "Heterodimerization of the transcription factors E2F-1 and to cooperative trans-activation."; Conges Dev. 7:1850-1861(1993). ************ WYSL YEAGT PSAJ.CAEEL TA10_ARAYH SPPA_HAEIN LTEL YEAGT CTOCHUMAN DYBC_CAEEL PAEE_ECOLI CLPE_ECOLI CLPE_ECOLI CLPE_ECOLI TCPL_HOUSE TCPL_HOUSE TCPL_CRIGR Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. factors 82F-1 and DP-1 leads partner 1) (DRTF1-P08964 P08989 P158129 P17866 Q14008 Q14000 P11984 P11984 6 saccharomyc 8 homo sapien 0 ceenorhabdi 1 escherichie 3 escherichie 4 mus musculu 3 mus musculu 9 cribetulus caenorhabdi arabidopsis haemophilus

Result

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Post-processing: Minimum Match 09
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Listing first 45 summaries

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105224 seqs, 38719550 residues

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MEDILING-93188967: PubMed-8446173;
Girling R., Partridge J.F.,
Girling R., Partridge J.F.,
Hsuan J.J., la Thangue N.B.;
*A new component of the transcription factor DRTP1/E2F.*;
Nature 362:83-87(1993).
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INTE: 18902: ...
InterPro; IPR003316; E2F_TDP.
Pfam; PF02319; E2F_TDP; I.
Transcription regulation; DNA-binding; Activator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of BIOInformatics and the ENGL outstaction the European BiOinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this Statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Transcription factor DP-1 (E2P dimerization partner 1) (DRTF1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIVACO
NIVACO
NIVACO
NIVACO
DEVELOPMENTAL EXPRESSION. MEDILINE-98025478; PubMed-9376316;
                         Girling R.;
Summitted (JUL-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                 Bukaryota, Metazoa,
Mammalia, Eutheria,
                                                      REVISIONS TO C-TERMINAL.
                                                                                                                                                        NCBI_TaxID-10090;
                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                          163
                                                                                                                                                                                                                                                                                                                                     BRAIM, PLACENTA, LIVER AND KIDNEY, LOWER LEVELS IN LUNG PANCREAS, NOT DETECTED IN HEART, INDICTION: DOWN-REGULATED DURING DIFFERENTIATION, PHOSPHORYLATION BY E2F-1-BOUND CYCLIN A-CDK2, IN THE
                                                                                                                                                                                                                                                                                                                                                                                   37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                        410 W;
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
                                                                                                                                                                 Chordata;
Rodentla;
                                                                                                                                                                                                                                                                                                                                                                                                                                        45070 MW;
                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 186; DB 1; 100.0%; Pred. No. 9.2e-19; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
DEF BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ASP/GLU-RICH (ACIDIC) (NCB DOMAIN).
PHOSPHORYLATION (BY CDK2) (POTENTIAL).
3FEEFELE49FD9ED0 CRC64;
                                                                                                                                                              Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENHANCES BINDING OF RB PROTEIN TO E2F POLY-PRO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIMERICATION (PCTENTIAL)
DCB1.
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                             410 M
                                                                                                                                                                                                                                                                                                                                                                                                      Length 410;
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       DOMAIN
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CC PUNCTION: CAN STRUILATE EST-EDEPHNOEMT TRANSCRIPTION. BINDS DIA COOPERATIVELY WITH ESP PANILY MEMBERS TRROUGH THE 22 RECOGNITION CC SITE, TTTCC/GCGC, POUND IN THE PROMOTER REGION OP A MUMBER OP GENES WHOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REGULATION OF GENES WHOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REGULATION OF IN DIA REPLICATION. THE 6P2/22F COMPLEX FUNCTIONS IN THE COMPLEX COMPONENT OF THE DYSLYZE TRANSCRIPTION PACTOR COMPLEX COMPONENT OF THE DYSLYZE TRANSCRIPTION AND APOPTOSIS.

CC 1- SUBUNIT: COMPONENT OF THE DRIFT/ESP TANSCRIPTION AND APOPTOSIS.

CC 1- SUBUNIT: COMPONENT OF THE DRIFT/ESP TANSCRIPTION AND APOPTOSIS.

CC 1- SUBUNIT: COMPONENT OF THE DRIFT/ESP TOM PROTEIN REI AND FOREIN REI AND APOPTOSIS.

CC 1- SUBUNIT: COMPONENT OF THE DRIFT/ESP TANSCRIPTIONALLY ACTIVE. VIRAL ORCOPROTEINS, NOTABLY ZIA, T-ANTIGEM AND HYP E7, ARE CAPABLE OF SEQUESTERING ARE PROTEIN, THUS RELEASING THE ACTIVE COMPLEX.

CC 1- SUBURITIALIZ IN THE INTESTINAL EPITHELLUM, FIRST EXPRESSED OF SEQUESTERING ARE PROTEIN, THE STRUELLAGE ENTRELISURS, LEVELS IN THE INTESTINAL SEPTHELLAGE.

CC 11 SUBCELLULAR ACCASION: MOLESE FOR THE ACTIVE COMPLEX.

CC 12 SO THE MESSENTIAL SEPTHELIAL COMPARMENT. HITH EXTRELION INCREASES

CC SUBSTANTIALIZ IN THE INTESTINAL EPITHELIUM WITH LOWER LEVELS IN THE INTESTINAL SEPTHELIAL COMPARMENT. HITH SETHELIAL DIFFERENTIAL SEPTHELIAL COMPARMENT. HITH SETHELIAL DIFFERENTIAL SEPTHELIAL COMPARMENT. HITH SETHELIAL SEPTHELIAL SEPTHELIAL COMPARMENT. HITH SETHELIAL SEPTHELIAL COMPARMENT. HITH SETHELIAL SEPTHELIAL SEPTHELIAL COMPARMENT. HITH SETHELIAL SEPTHELIAL SEPTHELIAL COMPARMENT. HITH SETHELIAL SEPTHELIAL SEPTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: X72310; CAA51056.1;
HSSP; Q14188; 1CP7.
MCD; MGI:101934; Tfdp1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PRO? entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMB outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commarcial entities requires a licegae agreement (see http://www.isb-sib.ch/announce/or send an email to licement sib.ch).
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Cell Growth Differ. 8:53-563(199).
-I- FUNCTION: CAN STIMULATE E2F-DEPENDENT TRANSCRIPTION. BINDS DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97294022; PubMed-9149906; Dagnino L., Fry C.J., Bartley S.M., Phillips R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Expression patterns of the E2F family of transcription factors during mouse nervous system development.";
mech. Dev. 66:13-23(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR003316; E2F_TDP.
Pfom; PF02319; E2F_TDP; 1.
Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dagnino L., Fry C.J., Bartley S.M., Farnham P., Gallie B.L., Phillips R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                cycle.
DIMERITATION (POTENTIAL).

CC81.

DCB2.

ASP/GLU-RICH (ACIDIC) (NCB DOMAIN).

PHOSPHORYLATION (BY CDM2) (POTENTIAL).

; PERAO90C78107189 CRC64;
                                                                                                                                                                                                                                                                                                                            POTENTIAL.
DEP BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Farnham P., Gallie B.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear protein;
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8

Query Match 100 Best Local Similarity 100 Matches 37; Conservative

100.01;

Score 186; DB 1; Pred. No. 9.2e-19; ; Mismatches 0;

Length 410; Indels

0 Gaps

0

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W *-RAY CRESTALLOGRAPHY (2.6 ANGSTROMS) OF 121-215.

W **REDINE-99190701; PUDM60-1090723;

LA Zheng M., Fraenkel E., PADO C.O., Pavletich N.P.;

Thrusture-19190701; PUDM60-1090723;

LA Zheng M., Fraenkel E., PADO C.O., Pavletich N.P.;

Thrusture-19190701; Pudm60-10907;

Thrusture-191907;

LA COPERATIVELY WITH E2F PAMILY MEMBERS TRANSCRIPTION. BINDS DNA COOPERATIVELY WITH E2F PAMILY MEMBERS THROUGH THE E2 RECOGNITION COMPOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REGULATION OR IN COOPERATIVELY WITH E2F PAMILY MEMBERS THE CONTROL OF COMPOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REGULATION OR IN COOPERATIVELY BOTH CELL PROLIFERATION AND APOPTOSIS.

CC ONA REPLICATION. THE DP3/CEP TRANSCRIPTION PACTOR COMPLEX COMPOSES OF THE COMPOSE CAN INTERACT WITH HYPOPHOSHORYLATED TRANSCRIPTION PACTOR COMPLEX COMPOSES OF TRANSCRIPTION PACTOR COMPLEX COMPOSES OF TRANSCRIPTION PACTOR COMPLEX COMPOSES OF TRANSCRIPTION DOMAIN. DURING THE CELL TRAILITY THE E2F TRANSCRIPTION PACTOR COMPLEX COMPOSED OF TRANSCRIPTION DOMAIN. DURING THE CELL TRAILITY THE E2F TRANSCRIPTION DOMAIN. DURING THE COMPLEX CYCLE, RESCONSE OF TRANSCRIPTION DOMAIN. DURING THE CELL TRAILITY THE E2F TRANSCRIPTION DOMAIN. DURING THE COMPLEX RESCONSE OF TRANSCRIPTION DOMAIN. DURING THE CELL PROJECT OF TRANSCRIPTION. DURING THE CELL PROJECT OF TRANSCRIPTION. DURING THE CELL PROJECT OF TRANSCRIPTION.
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Q1418B; Q14187; Q13331;

F 15-7UL-1996 (Rel. 39, Last sequence update)
F 30-MAY-2000 (Rel. 39, Last sequence update)
F 16-OCT-2001 (Rel. 40, Last annotation update)
F 72-OCT-2001 (Rel. 40, Last annotation update)
F 72-OCT-2001 (Rel. 40, Last annotation partner 2).
F 72-OCT-2001 (Rel. 40, Last annotation partner 2).
F 72-OCT-2001 (Rel. 40, Last annotation partner 2).
F 16-OCT-2001 (Rel. 39, Last sequence update)
F 16-OCT-2001 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-102 FROM W.A. (ALPHA ISOFORM).

Thang Y., Chelluppan S.P.,

"Transcriptional activation and expression of DP transcription
factors during cell cycle and TPA-induced U937 differentiation.
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 62-79 FROM M.A. (DELTA ISOFORM), AND ALTERNATIVE SPLICING. TISSUE-SEASTHOCYCES; NEDLINE-96353662; PubMed-8755520; M.H., Phillips R.S., Horowitz J.M.; Progers K.T., Higgins P.D.R., Mills M.M., Phillips R.S., Horowitz J.M.; *DP-2, a heterodineric partner of E2P: identifycation and characterization of DP-2 proteins expressed is a five of the progeness 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95303470; PUDMAG-7784053; Fhang Y., Chellappan S.P.; *Cloning and characterization of human partner of E2P.; *Oncogene 1077005-2093(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (DELTA ISOPORM), AND CHARACTERIZATION. MEDILINE-95257935; Pubhed-7739537; MI C.L., Sukerberg L.R., Myvu C., Harlov E., Lees J.A.; "In vivo association of E2F and DP family proteins."; Nol. Cell. Biol. 15:2536-2546(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DP2, a novel dimerization
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EMBL; U.40386; AAA69016.1; -.
EMBL; U.18422; AAB60378.1; -.
EMBL; U.75488; AAB7321.1; -.
EMBL; U.5117; AAC50642.1; -.
POB; 1CF7; 02-APR-99.
TRANSFAC; T03000; -.
                                                                                                                                                                                                            NIM; 602160; ...

InterPro; IPR003316; B2F_TDP,

InterPro; IPR003316; B2F_TDP,

Pfam; pr02319; E2F_TDP; 1.

Transcription regulation; DNA-binding; Activator; Nuclear protein;

Transcription regulation; DNA-binding; Activator; Nuclear protein;

Prosphorylation; Coll cycle; Alternative splicing; 3D-structure,

Phosphorylation; Coll cycle; Alternative splicing; 3D-structure,

Phosphorylation; Coll cycle; Alternative splicing; 3D-structure,

Phosphorylation; Coll cycle; Alternative splicing; 3D-structure,

DNA_BIND 17c 210 DEF BOX.
                               VARSPLIC
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bidinformatics and the EMB outstation - the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions so long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licensessisb-sib.ch).
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SEQUENCE
                                                                                      VARSPLIC
                                                                                                                       VARSPLIC
                                                                                                                                             COLRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGH LEVELS IN HEART AND SKELETAL MUSCLE. ALSO FOUND IN PLACENTA, KIDNEY, BRAIN, LUNG AND LIVER. THE PRESENCE AS WELL AS THE ABUNDANCE OF THE DIFFERENT TRANSCRIPTS APPEAR TO VARY SIGNIFICANTLY IN DIFFERENT TISSUES AND CELL LINES.

PTM: PHOSPHONYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUESTERING RB PROTEIN, THUS RELEASING THE ACTIVE COMPLEX. SUBCELLULAR LOCATION: MUCLEST.
ALTERNATIVE PRODUCTS: AT LEAST 4 130FORMS; ALPHA/49 KDA (SHOWN HERE), BETA/43 KDA, GAMMA AND DELTA/48 KDA: MAY BE PRODUCED BY
146 27
                                   64
                                                                                      103
                                   173
                                                                                                                  4401222
49236 MN;
                                                                            DIMERIZATION (POTENTIAL).

DCB1.

DCB2.

DCB2.

ASP/GLG-RICH (ACIDIC) (NCB DOWAIN).

PHOSPHORYLATION (BY CDK2) (POTENTIAL).

PHOSPHORYLATION (BY CDK2) (POTENTIAL).

MISSING (IN ISOFORM BETA, ISOFORM GAMMA AND ISOFORM DELTA).

MISSING (IN ISOFORM BETA AND ISOFORM
                                   AND ISOFORM DELTA).
MISSING (IN ISOFORM BETA AN
GAMMA).
S -> SQ (IN ISOFORM GAMMA).
I -> T.
/FTId=VAR_002272.
19A6C85BAD61DFF1 CRC64;
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몽
                                                                                DP_DROME STANDARD; PR
C 024318; PR
T 15-7UL-1996 (Rel. 36, Created)
T 15-7UL-1998 (Rel. 37, Last sequent
T 15-DEC-1998 (Rel. 37, Last annot
prosophila melanogaster (Fruit fly).

Elkaryota: Metazoa: Arthropoda: Trachesta: Hexapoda: Insurerygota: Moptera: Endopterygota: Diptera: Brachycera: Ephydroidea: Drosophildae: Drosophila.

NCBI_TexID-7237;

[1]
                                                                         Transcription
                                                                                                                                                                            factor dp.
                                                                                   sequence u
                                                                                                                            PRT;
                                                                                  update)
on update)
                                                                                                                            377
                                                                                                                            ζ
                                  Muscomorpha;
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Query Match Best Local S Matches 37

Similarity 37; Conserv

100.0%; ilarity 100.0%; Conservative 0

0

Score 186; DB 1; Pred. No. le-18; ; Mismatches 0;

Length 446; Indels

<u>.</u>

والمعترض المراجع والمراجع والمالي

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Ouery Match 89.2%;
Best Local Similarity 86.1%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDPH_CAREL STANUARD,
TDPH_CAREL STANUARD,
022703;
15-UTL-1996 (Rel. 36, Created)
10-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-1001 (Rel. 39, Last annotation update)
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstaction the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license spreement (see http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metaroa; Nematu
Rhabditidae; Peloderinae;
RCBL Taxib-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0011763; Dp.
InterPro; IPR003116; E2F_TDP.
Pfam; PF02319; E2F_TDP; 1.
Transcription regulation; DNA-binding; Nuclear protein DOMAIN
81 89 POLY-SER.
SEQUENCE 377 AA; 42683 MM; 868F180D243C3DDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94294381; PubMed-8022787;
Dynlacht 8., Brook A., Dembski M., Tenush
"DM-blading and trans-activation properti
                                                                                                                                                                                                                               REVISIONS.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM M.A.
STRAIN-BRISTOL NZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X79708; CAA56147.2; ALT_INIT.
H93P; Q14188; ICP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Eye imagin
                                                                                                                                                                                                                                                                                          Submitted (DEC-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. Natl Acad. Sci. U.S.A. 91:6359-6363(1994).

FUNCTION: CAN STINULAME EXP-DEPENDENT TRANSCRIPTION.

SUBUNIT: HETERODINER OF ZEF AND DP. COOPERATE TO GIVE SEQUENCE-
SPECIFIC DNA BINDING AND OPTINAL TRANS-ACTIVATION,

SUBCELULAR LOCATION: Nuclear (Potential).

SIMILARITY: BELONGS TO THE EZF/DP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                           ans.
Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disk;
                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 166; DB 1;
Pred. No. 5.6e-16;
4; Mismatches. 1
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                                                                                                                         RETISSUE-SEAN, and ALTERNATIVE SPLICING.

RETISSUE-SEAN, and Kidney;

RY TISSUE-SEAN, and Kidney;

RX MEDLINE-S003891; PUNNEd-7178568;

RX OTTONOTOMY E., De La Lune S., La Thangue N.B.;

RY A new member of the DP family, DP-J, with distinct protein products at respects a regulatory role for alternative splicing in the cell cycle at transcription factor DRTP1/C2P, ";

RO OTTONIC CAN STHULLATE E2P-DEPENDENT TRANSCRIPTION. BINDS DNA COMPERATIVELY WITH E2P FAMILY MEMBERS THROUGH THE E2 ARCOGNITION OR IN COMPERATIVELY WITH E2P FAMILY MEMBERS THROUGH THE E2P-1/DP CONFICE OF GENES WHOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REGULATION OR IN COMPERS TO MEDIATE BOTH CELL PROLIFERATION AND POPTOSIS.

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE E3P-1/DP COMPEX OF COMPLEX CAN PRESENT ON MEDIATE BOTH CELL PROLIFERATION AND APOPTOSIS.

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE E3P-1/DP COMPLEX CAN PORMS HETERODILERS WITH E2P FAMILY MEMBERS. THE COMPLEX CAN PORMS HETERODILERS WITH E2P FAMILY MEMBERS. THE COMPLEX CAN PORMS HETERODILERS WITH E2P FAMILY MEMBERS. THE COMPLEX CAN PORMS HETERODILERS WITH E2P FAMILY MEMBERS. THE COMPLEX CAN PROLIFE DITY AND P1301 THAT INHIBIT THE E2P COMPLEX.

CC THATERIFICATION OF THE DETTY AND HEAVEN PROMITES PROMITED IN WINDLESS FOR THE COMPLEX.

CC DRTPL/E2P COMPLEX. REPRODUCES RETINGING THE COMPLEX.

CC PROSPRIBLES AND DELTA; ARE PRODUCED BY ALTERNATIVE SPELICING.

CC PINIES SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED. HIGHEST COMPLEX CAN PASE, PHASE, PHASE,
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15-JUL-1998
30-NAY-2000
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30-NAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription factor DP-2 (R2F dimerisation pt
TPDP2 OR DP2.
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InterPro: IPR003316; E2F_TDP.
Pfam; P503319; E2F_TDP; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: 158319; CAA92699.1;
HSSP: Q14188; 1CF7.
WormPep; 723G7.1; CE03702
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Manmalia; Eutheria; Rodentia;
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75.7%;
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; Pred. No. 6.3e
7; Mismatches
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5.3e-14;
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requires a license agreement (See)

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Query Match
Best Local Similarity 67.6
Matches 23: Conservative
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054917;
30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
16-0CT-2001 (Rel. 3
                                                                                       MEDILINE-98065940: PubMed-9403682;

MOTRE! M., Wenkel J., Bannister A.J., Kouzarides T., Hagemeist C.;

MATRE! M.K et repressor of transcription.";

AN EZP-11Ke repressor of transcription.";

AN EXP-11Ke repressor of transcription. BINDS DNA.

COOPERATIVELY WITH DP PROTEINS THROUGH THE EZ RECOGNITION SITE.

TYPICC/GCGC. HAS A PREFERNCE FOR THE TYPICCGC ELF RECOGNITION SITE.

TYPICC/GCGC. HAS A PREFERNCE FOR THE TYPICCGC ELF RECOGNITION SITE.

(BY SINILARITY). EXHIBITS MO TRANSACTIVATION ACTIVITY. APPEARS 70

REQUIATE A SUBSET OF E2F-DEPENDENT GENES WHOSE PRODUCTS ARE

REQUIRED FOR ENTRY INFO THE CELL CYCLE BUT NOT FOR MORMAL CELL

CYCLE PROGRESSION. OVEREXPRESSION DELAYS THE EXIT OF CELLS FROM

THE S-PHASE (BY SINILARIY).

1- SUBJULT: COMPONET OF THE DEPENDENT.

SUBJULT: COMPONET OF THE DEPENDENT.

1- SUBJULT: COMPONET OF THE DEPENDENT.

1- SUBJULT: COMPONET OF THE DEPENDENT.

1- SINILARIY: BELOWS TO THE E2F TRANSCRIPTION FACTOR COMPLEX.

1- SINILARIY: BELOWS TO THE E2F TRANSCRIPTION FACTOR COMPLEX.

1- SINILARIY: BELOWS TO THE E2F TRANSCRIPTION FACTOR COMPLEX.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outsteation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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HSSP; Q14108; 1CP7.
HSD; MG1:107167; Tfdp2.
InterPro; IPR003316; E2F_1
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DNA_BIND 129
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Pfam; PF02319; E2F_TDP: 1.
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Rel. 39. Last aequence update)
Rel. 40. Last annotation update)
[actor E2F6 (E2F~6) (E2F~binding site modulating
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Pred. No. 2.3e-05;
1; Mismatches 1.
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Sciurognathi; Nuridae; Murinae; Mus
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Homo sapiens (Human).
Eukaryota; Mecazoa; Ch
Mammalls; Eutherla; Pr
MCBI_TaxID=9606;
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HEDLINE-98356131, PubMed-9689056;

GAUDALE S., Mood J.G., Livingston D.M.;

"Unusual proliferation arrest and transcriptional

"Unusual proliferation arrest and transcriptional

of a newly discovered EZP family member, EZP-6.";

Proc. Natl. Acad. Sci. U.S.A. 95:9190-9195(1998).
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HSSP; 016254; 1CF7.
                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJINE-98368625; PubMed-9704927; Carteright P., Mueller #: Wagener #E2P-6; a novel member##f the E2P f dependent transcription, "; Oncogene 17:611-623(1998).
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NGD; MGI:1354159; E266.
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or send an email to license@isb-sib.ch).
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MEDLINE-98169460; PubMed-9501179;
Trimarchi J.M., Fairchild B., Verona
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c. Natl Acad. Sci. U.S.A. 95:2850-2855(1998).
c. Natl Acad. Sci. U.S.A. 95:2850-2855(1998).
pronction: INHIBITOR OF E2F-DEPENDENT TRANSCRIPTION. BINDS DNA POUNCTION: INHIBITOR OF E2F-DEPENDENT TRE TRECOGNITION STRE TYTCC/GCGC. HAS A PREFERENCE FOR THE TYTCC/GCGC. HAS A PREFERENCE FOR THE THYOTEIN AND POCKET PROTEIN BINDING DOMAINS. APPEARS TO REQULATE A SUBSET OF E2F-DEPENDENT GENES WHOSE PRODUCTS ARE REQUIRED FOR ENTRY INTO THE CELL CYCLE BUT NOT FOR NORMAL CELL CYCLE PROGRESSION.
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|5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING TO CO-REPRESSORS (PROBABLE).
POTENTIAL.
DEF BOX.
DIMERIZATION (POTENTIAL).
LEUCINE-TIPPER.
TRANSCRIPTION REPRESSION DOMAIN
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
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                                                                                                                                                                                                                                                                              R., Moberg K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        R., Helin K.,
an inhibitor
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                                                                                                                                    SITE
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Best Local Similarity 48.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: AF059292; AAC31426.1; ...
EMBL; AF06138; AAC14694.1; ...
HSSP; Q16254; ICF7.
MIM; 602944; ...
InterPro; IPR003316; E2F_TDP.
Pfam; PF03319; E2F_TDP; 1.
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CONFLICT
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SEQUENCE
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                                                                                                                                                                         (1)
SEQUENCE FROM N.A.
STRAIN-SWISS ALBINO;
MEDILINE-54119858; Pubmed-8114719;
Plannky J.E., Myers D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; DNA-binding; Repressor; Nuclear protein; Cell cycle.
DEVELOPMENTAL EXPRESSION.
MEDILINE-98025478; PubMed-9376316;
Dagnino L., Fry C.J., Bartley S.M., Farnham P., Gallle B.L.,
                                                                                                            *Cloning, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGEN
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                          MCBI_TaxID-10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 KRRYDITHYLDGIDLYZKKSKNHIRWIG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 RRRVYDALNVLMAMNIISKE-KREIKWIG 31
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SUBURIT: COMPONENT OF THE DRTF1/E2F TRANSCRIPTION FACTOR COMPLEX.
FORMS HETERODIMERS WITH DP FAMILY MEXBERS.
SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION: Nuclear.
T15SUE SPECIFICITY: EXPRESSED IN ALL T1SSUES EXAMINED. HIGHEST
LEVELS IN PLACEMA, SKELETAL MUSCLE, HEART, OVARY, KIDNEY, SMALL
INTESTINE AND SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
                                                                                                            chromosomal location, and characterization of mouse E2F1.^{+}, Biol. 14:1861-1869(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.0%;
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129
164
268
268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ĩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 72.5; DB 1; Length 281; Pred. No. 0.0066; 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L->E: REDUCTION IN REPRESSOR ACTIVITY,
LITTLE EFFECT ON S-PHASE ENTRY.
AR -> HE (IN REF. 3).
I -> V (IN REF. 3).
G -> E (IN REF. 3).
539E049C15AD3508 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSCRIPTION REPRESSION DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
DEP BOX.
DIMERIZATION (PCTENTIAL).
                                                                                                                                                                                           Drinkwater N.R., Kaelin W.G.,
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                                                                                       Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phillips R.A.; Expression patterns of the E27 family of transcription factors during mouse nervous system development."; Mech. Dev. 66:13-25(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-98337455; PubMed-9674698;
HOlnberg C., Helin K., Sehested M., Karlatroem O.;
"EZF-1-induced p53-independent apoptosis in transgenic mice.";
Oncogene 17:143-155(1998).
-1- FUNCTION: TRANSCRIPTION ACTIVATOR THAT BINDS DNA COOPERATIVELY
                                                                                                                                                                                                                                           EMBL: L21973; AAA83217.1; -. HSSP: Q16254; 1CF7. TRANSPAC: T00219; -. TRANSPAC: T01543; -. TRANSPAC: T01543; -. TRANSPAC: T01543; -. T
                                                                                                                                                                      MGD; MGI:101941; E2f1.
InterPro; IPRODJ316; E2;
Pfam; PF02319; E2F_TDP;
Transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - i - SINILARITY: BELONGS TO THE E2F/DP FAMILY.
SEQUENCE
430
                                                                                                         1; E41...
)0316; E2P_TDP.
)03116; E2P_TDP:
; E2P_TDP: 1.
regulation; Activator; DNA-binding; Nuclear protein;
regulation; Activator; DNA-binding; Nuclear protein;
con; Cell cycle; Apoptosis.
CYCLIN A/CDK2 BINDING (POTENTIAL).
169
169
189
279
430
                                                                                                                                                                                                                                         :
 ₹
                               LEUCINE-ZIPPER.

DEP BOX.

DIMERIATION (POTENTIAL).

TRANSACTIVATION (POTENTIAL).

RETINOBLASTOMA PROTEIN RB1 BINDING
C5DF18AD3B4DFEFA CRC64;
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38.44;

Score 71.5;

DB 1;

Length 430;

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RESULT 10
E2F1_HUWAN STANDARD;
ID E2F1_HUWAN STANDARD;
AC Q01094; Q92768; Q13143;
DT Q1-JUL-1993 (Rel. 26, Lesi
AP SEQUENCE PROM H.A.

AD Deloukas F., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

AD Deloukas F., Matthews L.H., Ashurst J., Babbege A.K., Bagguley C.L.,

Balley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

AD Besiley J., Barlow K.F., Bakey S.E., Bridgeman A.M., Brown A.J.,

Besiley J., Burtil W., Buther A.P., Carder C., Carter N.P.,

AL, Chapman J.C., Clamp M., Clark G., Clark L.M., Clark S.Y., Clee C.M.,

AL, Chapman J.C., Clamp M., Clark G., Clark L.M., Clark S.Y., Clee C.M.,

AL, Clegg S., Cobley V.E., Collier R.E., Connor K., Corby N.R.,

AL, Collson A., Coville G.J., Deadman R., Dhami F., Dunn M.,

AL, Collen A., Coville G.J., Deadman R., Dhami F., Dunn M.,

AL, Collien A., Coville G.J., Deadman R., Dhami F., Dunn M.,

AL, Collson A.G., Frankiand J.A., Freser A., French L., Garner P.,

AL, Collen A., Coville G.J., Hosth P.D., Hos., Holden J.L., Howden P.J.,

AL, Collen D.Y., Griffiths C., Griffiths M.N.D., Gwilliam R., Hollen P.J.,

AL, Haumond S., Harley J.L., Heath P.D., Hos., Holden J.L., Howden P.J.,

AL, Halley B., Hunt A.R., Hunt S.E., Jecosch K., Johnson C.M., Johnson D.,

AL, May M.P., Kimberley A.M., King A., Knighte A., Laird G.K., Lavlor S.,

AL, Lavlor S.L., Hecombehle L.J., McLey K., McNurray A.A.,

AL, Milne S., Mistry D., Hoore M.J.F., Mullikin J.C., Mickerson T.,

RA, Oliver M., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 43. Watches 14; Conservative
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Eukaryota: Metazos; C
Mammalia: Eutheria: F
MCBI_TaxiD=9606;
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HEDLINE-92146720; PubMed-1638634;
Helin K., Lees J.A., Vidal N., Dyson N.J., Harlow E., Fattaey
Helin K., Lees J.A., Vidal N., Dyson N.J., Harlow E., Fattaey
*A cDNA encoding a pRB-binding protein with properties of the
transcription foctor E2P.*;
Cell 70:337-350(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE PROM B.A.
MEDLINE-97082961; PubMed-8984493;
Neuman E., Sellers W.R.S., MCNeil J.A.,
Kaelin W.G. Jr.;
"Structure and partial genomic sequence
gene 171:163-169(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM M.A.

MEDLINE-92346721; PubMed-1538635;

RABLIN W.G. Jr., Krak W., Sellers W.R., Decaptio

RABLIN W.G. Jr., Krak W., Sellers W.R., Decaptio

Puchs C.S., Chittenden T., Li Y., Farnham P.J., B

Fuchs C.S., Chittenden T., Li Y., Farnham P.J., B

Livingston O.M., Flemington E.K.,

*Expression cloning of a cDNA encoding a retinoble

Protein with E2F-like properties.*;

Cell 70:351-364(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein 1) (RBAP-1).
E2F1 OR RBBP3.
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1-JUL-1993 (Rel. 26, Lest sequence update)
1-MR-2002 (Rel. 41, Lest annotation update)
1-MR-2002 (Rel. 26, Lest annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159
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Primates;
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8; Mismatches
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Blanar M.A.,
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; Homo.
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TRANSCTIVATION INHIBITION.

TO TRANSCTIVATION INHIBITION.

Y MEDLING-94019324, Pubmed-8413249;

X HEDLING-94019324, Pubmed-8413249;

X HEDLING-94019324, Pubmed-8413249;

X HELLING-94019324, Pubmed-8413249;

X "Inhibition of E2F-1 transactivation by direct binding of the retanoblastoma protein.";

Y "Inhibition of E2F-1 transactivation by direct binding of the retanoblastoma proteins.

X "I FUNCTION: TRANSCRIPTION ACTIVATOR THAT BINDS DNA COOPERATIVELY WITH DP PROTEINS THROUGH THE PROCESSION OF A NUMBER OF GENES WHOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REQUILATION OR IN DNA REPLICATION. THE DRIPPIPE COMPLEX FUNCTIONS IN THE CONTROL OF CELL-CYCLE PROCRESSION FROM G1 TO S PHASE. E3F-1 BINDS PREFERRITILLY RB1

PROTEIN, IN A CELL-CYCLE DEPENDENT MANNER. IT CAN MEDIATE BOTH
                                                                                                                                                                                                                                                                                                                                                                                             INIBITION OF DNA-BINDING.

INIBITION OF DNA-BINDING.

MEDILINE-95059071; PubMed-7969176;

Yu M., Sheppard K.-A., Peng C.-Y., Yee A.S., Pi.

You M., Sheppard K.-A., Peng C.-Y., Yee A.S., Pi.

You M., Sheppard K.-A., Peng C.-Y., Yee A.S., Pi.

You M., Sheppard K.-A., Peng C.-Y., Yee A.S., Pi.

No., Sheppard K.-A., Peng C.-Y., Yee A.S., Pi.

L. Mol. Cell. Biol. 14:8420-8431(1994).
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                                                                                                                                                                                                                                                                                                                     PUNCTION IN APOPTOSIS. 4
MEDILINE-99234788; PubMed-8170934;
Wh X., Levine A.J.;
"P53 and E2F-1 cooperate to media"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIFFERENTIAL REGULATION BY CYCLIN/CDK2 KINASES.
MEDLINE-95047332; PubMed-7958855;
Bynlacht B.D., Flores O., Lees J.A., Harlow E.;
*Differential regulation of E2F transactivation complexes.";
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MEDLINE-94306513; PubMed-8033208;

MIEDLINE-94306513; PubMed-803208;

Miedline-94306513; PubMed-803208;

Mivingston D.M.;

Livingston D.M.;

Livingston D.M.;

Negative regulation of the growth-promoting transcription f

"Negative regulation of the growth-promoting transcription f

E2F-1 by a stably bound cyclin A-dependent protein kinase.";

Cell 78:161-172(1994).
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Taya Y., Nishimura S., Okuyama A.,
"Phosphorylation of 83F-1 by cyclin
Oncogene 10:229-236(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-111 PROM M.A.

MEDILINE-95047311; PROMHOM-7958836;

MEDINE-95047311; PubMed-7958836;

MINORSON D.G., Ohteni K., Nevins J.R.;

MINORSON D.G., Ohteni K., Nevins J.R.;

Antoregulatory control of E3F1 expression in response and negative regulators of call cycle progression.";

Genes Dev. 8:1514-1525(1994).
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                                                                                                                                                                                                                                                                                                  "953 and E2F-1 cooperate to mediate apoptosis.";
Proc. Natl. Acad. Sci. U.S.A. 91:3602-3606(1994).
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MEDLINE-97342624; PubMed-919931.
Dynlacht B.D., Moberg K., Lees J.A., Harlow
"Specific regulation of E2F family members b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95140413;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibits the DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by cyclin-dependent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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CELL PROLIFERATION AND P33-DEPENDENT APOPTOSIS.

- SUBURIT: COMPONENT OF THE DRYFI/ESP TRANSCRIPTION PACTOR COMPLEX. BORNS HETERODIMERS WITH DP FAMILY MEMBERS. THE ESF-1 COMPLEX BINDS SPECIFICALLY HYPOPHOSPHORYLATED RETIMOBLASTOMA PROTEIN RB1. DURING THE CELL CYCLE, RB1 BECOMES PHOSPHORYLATED IN MID-TO-LATE G1 PHASE, DETACHES FROM THE DRYFI/ESF COMPLEX, RENDERING ESF TRANSCRIPTIONALLY ACTIVE. VIRAL ONCOPROTEINS, NOTABLY ELA, TAMPIGEN AND HPY E7, ARE CAPABLE OF ERQUESTERING RB PROTEIN, THUS RELEASING THE ACTIVE COMPLEX.

--- SUBCELLULAR LOCATION: NUCLEBY.

--- SINGLEAVELAR DECOMES TO THE ESF/DP PAMILY.

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RESULT 11
E2F1_CHICK
                                                                                                                                                                                                                                                                                          Query Match 38.4
Best Local Similarity 43.6
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licensee1sb-sib.ch).
                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
SEQUENCE
EZEL_CHICK STANDARD; PRT; 403 AA. 059977; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 7renscription factor EZFI (EZF-1). EZFI. Callus gallus (Chicken).
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                                                                                                                      4 RRRYDALNYLMAMNIISKE-KREIKWIGLPT 34
:||:|| || : :|:|: | |:|:| |
164 KRRITDITNYLEGIQLIAKKSKNHIQWLGSHT 195
                                                                                                                                                                      38.44;
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                                                                                                                                                            Score 71.5; DB
pred. No. 0.015;
8; Mismatches
                                                                                                                                                                                                            Y-C: NO RETINOBLASTOWA PROTEIN BINDING.
WRRICDLETDHOYLLESSCPARGR -> RTPGTPRRORRLCP
PRAPGRAPC (IN REF. 6).
S -> Y (IN REF. 4)...
N -> T (IN REF. 4)...
T -> N (IN REF. 4)...
1003B3F654F0C60DF CRC64;
                                                                                                                                                                                                                                                                                   RETINOBLASTOMA PROTEIN REL BINDING (POTENTIAL).
                                                                                                                                                                                DB 1: Length 437;
                                                                                                                                                              9; Indels
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RESULT 12
82F2_HUMAN
ID 82F2_H
AC Q14209
DT 01-NOV
DT 01-NOV

STANDARD;

137

℥

014209; 01-4209; 01-40V-1997 01-40V-1997

(Rel.

35, Created)
35, Last sequence update)
39, Last annotation update)

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                                                                                                                                 EMBL: X89245: CAA61533.1;

PR TRANSFAC: TO2951: -

PR Interpro; IPR003316: E2F_TDP.

PR Pfam: pP02318: E2F_TDP;

R Pfam: pP02318: E2F_TDP;

R Pfam: pP02318: E2F_TDP;

Phosphorylation; Cell cycle.

CYCLIN A/CDK2 BINDING (POTENTIAL).

TOMAIN 130 151 LECCINE-LEPPER.

TOMAIN 135 171 DEF BOX.

TOMAIN 172 361 DIMERIZATION (POTENTIAL).

TOMAIN 173 361 DIMERIZATION (POTENTIAL).

TOMAIN 173 361 DIMERIZATION (POTENTIAL).

TOMAIN 173 361 DIMERIZATION (POTENTIAL).

TOMAIN 175 392 RETINDELASTOMA PROTEIN RB1 BINDING
                                              Query Natch
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96038875; PubMed-7478572;
Pastesu S., Loiseau L., Arnaud L., Trembleau A., Brun G.;
"Isolation and characterization of a chicken homolog of the E2F-1
transcription factor.";
Oncogene 11:1475-1486(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Meognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBL_TaxID-9031;
                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not resmoved. Usage by and for commercial entities requires a license agreement (See http://www.isb-stb.ch/announce/or send an email to licensesisb-sib.ch).
4 RRRYYDALWYLADMNIISKE-KKEIKWIG 31
:||:|| ||| :|:|:| |:|:|:|
141 KRRIYDITNYLEGIQLITKKSKNNIQWLG 169
                                                37.9%;
nilarity 44.8%;
Conservative
                                                                                                          403 AA; 4359 MN;
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Pred. No. 0.01
8; Mismatches
                                                                                                              (POTENTIAL).
78EEA320537C33ED CRC64/
                                                              .019;
1 8d
                                                                           Length 403;
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                                                    Caps
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Transcription factor E2F2 (E2F-2)

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Query Match 37.4%;
Best Local Similarity 44.8%;
Matches 13; Conservative
                                                                                                                                                              Prenscription regulation; 65 DONAIN 65 DONAIN 107 DONAIN 155 DONAIN 160 DONAIN 197 DONAIN 360 DONAIN 360 DONAIN 360 DONAIN 360 DONAIN 410
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MEDILINE-94067141; PubMed-8246995;
IVEY-Hoyle H., Conroy R., Huber H.E.,
Heimbrook D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and characterization of E2P-2, a novel protein with the biochemical properties of transcription factor E2F."; mai. Cell. Biol. 13:7802-7812(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: L22846; AAA16890.1; ...
EMBL: AL021154: CAA15949.1; ...
HSSP: Q16254; ICF7.
TRANSFAC; T01544; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SHISS-PROY entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla, Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                 Pro; IPR003316; E2F_TDP.
Pr02313; E2F_TDP; 1
Cription regulation; Activator; DNA-binding; Nuclear protein;
horylation; Cell cycle.
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115 cycle.
196
176
176
197
289
363
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                                                                                                                      47505
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Score 69.5; DB 1; Length 437; Pred. No. 0.028: 7; Mismatches 8; Indels
                                                                                                                                                                                   LEGGINE-ZIPPER.
DEF BOX,
DIMERIZATION (POTENTIAL).
TRANSACTIVATION (POTENTIAL).
POLY-PRO.
                                                                                                                 RETINOBLASTOMA PROTEIN ASSOCIATION (POTENTIAL). 60541F4235507305 CRC64;
                                                                                                                                                                                                                                                                                                                               CYCLIN A/CDK2 BINDING (POTENTIAL).
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RESULT 13
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ID REPLY
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ID TO 15-JUL
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035261;
EMBL; AF015948; AAB71671.1; -. HSSP; Q16254; ICF7.
TRANSPAC, T02947; -. HGD; MGI:1096340; E2f3.
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Ξ. Gaps

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The pression patterns of the E2F family of transcription factors of trapression patterns of the E2F family of transcription factors of the patterns of the E2F family of transcription factors of the patterns of the E2F family of transcription factors of the family of transcription factors of the family of transcription factors of the family of the family of transcription factor family of the family of
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DEVELOPHENTAL EXPRESSION.

DEVELOPMENTAL E
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STRAIN-SMISS ALBINO; TISSUE-Fibroblast;
STRAIN-SMISS ALBINO; TISSUE-Fibroblast;
MEDLINE-SMOSJ478; pubMed-9376316;
Dagnino L., Fry C.J., Bartley S.M., Farnham P., Gallie B.L.,
Phillips R.A.;
"Expression patterns of the E2F family of transcription factors
during mouse nervous system development.";
during mouse nervous system development.";
hech. Dev. 66:13-25(1997).
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Eukaryota: Netazoa: Chordata:
Mammalia: Eucheria: Rodentia:
MACBI_TaxID~10090;
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166 KRRIYDITNYLEGIGLIRKKAKNNIGWYG
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on factor E2F3 (E2F-3) (Fragment).
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SESETTETE
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RA HOMITS N., Nagase T., Miyajima N., Sazuka T., Jaka S.;

RA HOMITS N., Nagase T., Miyajima N., Sazuka T., Jaka S.;

RA HOMITS N., Nagase T., Miyajima N., Sazuka T., Jaka S.;

RA Seki N., Kawatshayasi Y., Ishikawa K.*I., Tabuta S.;

RY "Prodiction of the coding sequences of unidentified human genes. II.

RY The Coding sequences of 40 new genes (KIAAOO4: KIAAOO8) deduced by the Coding sequences of unidentified human genes. II.

RY THE CODE OF THE PROPERTY OF THE PROPERT OF THE COOPERATIVELY WITH DP PROPEINS THROUGH THE EZ RECOGNITION SITE, TYTCC, CCCCC, POUND IN THE PROPEIR REGION OF A NUMBER OF GENES HOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REGULATION OF CELL-CYCLE DRYLOTIONS IN THE CONTROL OF CELL-CYCLE PROPERTY PER FOR GITO S PRASE, EZF-3 BINDS SPECIFICALLY TO RB1

PROPEIN, IN A CELL-CYCLE DEPENDENT HANNECRIPTION FACTOR COMPLEX BINDS COOPERATIVELY WITH DP-1 TO EJF SITES. INTERACTS HITH RETHOBLASTOMA PROPEIN RB1 AND RELATED PROFEINS (SUCH AS P107)

CONTROL PROPERTY THE EJF TRANSACTIVATION DOMAIN.

--- SUBURITY: BELLONGS TO THE EJF/OP FAMILY.
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Best Local Similarity 41.4
Watches 12; Conservative
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000716; Q15000;
01 NOV-1997 (Rel. 35, Lest sequence update)
01-NOV-1997 (Rel. 35, Lest sequence update)
16-OCT-2001 (Rel. 40, Lest annotation update)
Transcription fector E2F3 (E2F-3).
E2F3 OR KLAA0075.
E2F3 OR KLAA0075.
EARTH (MUMBA).
EARTH 
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Cell cycle.
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MEDLINE-94067142; PubMed-8246996;
Loss J.A., Soito M., Vidal M., Valentine M., Look T., Harlov E.,
Pyson N., Helin K.; Vidal M., Valentine M., Look T., Harlov E.,
"The retinoblastoms protein binds to a family of E2F transcription".
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by mon-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Bone marrow;
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Pfam; PP02319; E2F_TDP; 1.
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POTENTIAL,
LEUCINE-ZIPPER.
DEP BOX.
DIMERIZATION (POTENTIAL).
TRANSACTIVATION (POTENTIAL).
P130 PROTEIN ASSOCIATION (POTENTIAL).
P130 PROTEIN ASSOCIATION (POTENTIAL).
MH; 07BFCF4E0AOC8E77 CRC64;
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Pred. No. 0.031;
9; Mismatches 7;
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EMBL; D38550; BAA07553.1;
H55P; Q16254; LCF7.
MIN; 600427; -,
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Similarity
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                                                                                                           regulation; Activator; DNA-binding; Nuclear protein;
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DIMERIANTION (POTENTIAL).
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RETINOBLASTONA PROTEIN ASSOCIATION
(POTENTIAL).
4541365842CA99EC CRC64;
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POLY-ALA.
CYCLIN A/CDX2
POLY-GLY.
POTENTIAL.
                                               Pred. No. 0.041;
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(27386; 077035;
(27386; 077035;
01-WOY-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
7ranscription factor E2f (dE2F).
E2F OR E2F1 OR C66376.
E2F2 OR E2F1 OR C66376.
Euksryota; Hetazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Hetazoa; Arthropoda; Tracheata; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidea; Drosophila.

MCBI_TaxiD=7727;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE PROM N.A.

MEDLINE-9415893; PubMed-9114699;

Ohtani K., Nevins J.R.;

Functional properties of a Drosophila

Mol. Cell. Biol. 14:1603-1612(1994).
WEDLINE-99077992: PubMed-9858578; Sasaki T., Sawado T., Tamaguchi M., Shinomiya T.; Sasaki T., Savado T., Tamaguchi M., Shinomiya T.; Specification of regions of DNA replication initiation embryogenesis in the 65-kilobase DNApolalpha-dE2F locus melanogaster.*; melanogaster.*; Mol. Cell. Biol. 19:547-555(1999).
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TISSUS-Eye imaginal disk;
TISSUS-Eye imaginal disk;
MEDLINE-94794781; Pubmed-9022787;
MEDLINE-94794781; Pubmed-9022787;
DNA-bidding and trans-affication proproceins;
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STRAIN-OREGON-R;
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properties of Drosophila
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Hichards S., Ashburner M.A., Galle R.F.,
RA Brandon R.C., Morthan J.R., Yandell M.D., Ehang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blase) R.G., Champe M., Pfeliffer B.D.,
RA Burli J.F., Agbayani A., An H.-J., Andrews-Pfennkoch C., Baidwin D.,
RA Burli J.F., Agbayani A., An H.-J., Andrews-Pfennkoch C., Baidwin D.,
RA Burli J.F., Agbayani A., Berman B.F., Bhandari D., Belshakov S.,
RA Burkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burkis K.C., Busem D.A., Butler H., Cadiau E., Center A., Chandra I.,
RA Burkis K.C., Busem D.A., Butler H., Cadiau E., Center A., Chandra I.,
RA Gebon K.Y., Benus P.V., Berman B.F., Bhandari D., Belshakov S.,
RA Gebon K., Doup L.E., Downes H., Dayan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.R., Gu E., Gunn P., Harris H.,
RA Harris H.L., Harvey D., Halman T.J., Harranded J.R., Houck J.,
RA Harris H.L., Harvey D., Halman T.J., Harnison D., Katchim C.,
RA Kinmel B.E., Rodira C.D., Kraft C., Krarviz S., Kulp D., Lai E.,
RA Mcunt S.H., Holyhan R.V., Moberry C., Horris J., Hosbrefi A.,
RA Melson D.R., Welton K.A., Horland T.J., Wel M.-H., Holbed J.M.,
RA Neunt S.H., Holyhan R.V., Moberry C., Horris J., Hosbrefi A.,
RA Neunt S.H., Holyhan R.V., Moberry C., Horris J., Hosbrefi A.,
RA Neunt S.H., Holyhan R.V., Moberry C., Horris J., Hosbrefi A.,
RA Neunt S.H., Holyhan R.V., Moberry C., Horris J., Pan B., Shieb D., J.A.,
RA Neison D.R., Welson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Sylirsks R., Tector C., Turner R., Venter E., Wang A. H., Wang X.,
RA Sylirsks R., Tector C., Turner R., Venter E., Wang A. H., Wang X.,
RA Hardisher J., Shen B., Shoppin H., Shiba G., J., Ann M., Stang G., Jan D., J.,
RA Jenng X.H., Holyhan R., Jan M., Jang S., Tao Q.A.,
RA Hardisher J., Shiba G., Jan M., Shop G., Jang S., Tao Q.A.,
RA Hardisher S., Shiba G., Shoppin H., Shiba G., Jang G., Shiba H
Royzman I., Wh
"Mutations in
an associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEDLINE-98078671; PubMed-9418862;
Duronio R.J., Bonnette P.C., O'Farrell P.H.;
"Mutations of the Drosophila dDP, dE2P, and
distinct roles for the E2P-DP transcription
during the G1-S transition.";
Mol. Cell. Biol. 18:141-151(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medline-97415323;
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STRAIN-BERKELEY;
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Whittaker A.J., Orr-Weaver T.L.;
In Drosophila DP and E2P distinguish Gl-S progression from ted transcriptional program.*;
II:1999-2011(1997).
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PlyBase; Fbgn0011766; E2f.
InterPro; IPR003316; E2F_TDP.
Pfam; PP02319; E2F_TOP; 1.
Transcription regulation; DNA-b
Developmental protein; Activato
DNA_BIND 253 318 PO
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                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for compercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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EMBL; UJ0184; AAA19003.1: -

EMBL; AB011811: BAA12746.1: -

EMBL; AE003735; AAFS5904,1: -

HSSP; Q16254; 1CF7.
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                                                                                                                                 Activator
    ₹.
                                                                                                                                          DNA-binding; Nuclear protein;
DIMERIZATION (POTENTIAL).
POLY-SER.
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POLY-GLY.
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Search completed: August Job time: 222 sec 28, 2002, 13:03:16

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Query Match 36.3%; Best Local Similarity 48.1%; Matches 13; Conservative

Score 67.5; D Pred. No. 0.1; 6; Mismatches

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Maximum Match 1008
Listing first 45 summaries
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Meximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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l: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cgn2_6/ptodata/3/laa/5a_COMB.pep: 
/cgn2_6/ptodata/3/laa/5b_COMB.pep: 
/cgn2_6/ptodata/3/laa/6A_COMB.pep: 
/cgn2_6/ptodata/3/laa/6B_COMB.pep: 
/cgn2_6/ptodata/3/laa/f6B_COMB.pep: 
/cgn2_6/ptodata/A_COMB.pep: 
/cgn2_6/ptodata/A_COMB.pep: 
/cgn2_6/ptodata/A_COMB.pep: 
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11. Appl
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14. Appl
15. Appl
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17. Appl
18. Appl
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| US-08-836-582-2 | US-08-481-814A-8 | US-09-308-935-11 | US-08-481-814A-7 | US-08-136-119-2 | PCT-US93-11310-14 | US-08-139-937-14 | US-09-189-627A-13 | US-08-801-092-1 | US-08-462-174-3 | US-08-461-814A-6 | US-08-723-415B-13 | US-07-882-711-2 | -08-13 | -80 | 078-59 | 0S-08-428-131-12 | C. CE6. ROE - 60 - SO |
| Sequence 2, | Sequence 8, | Sequence 11 | Seguence 7, | Sequence 2, | Sequence 14 | Sequence 14 | Sequence 1: | Seguence 1, | Seguence 2, | Sequence 6, | Sequence 1: | Sequence 2, | Sequence 4, | Sequence. 9, | Sequence 1: | Sequence 12 | Sequence 5, |
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ALIGNMENTS

Sequence 1, Application US/09308939 Patent No. 6268334 GENERAL INFORMATION: APPLICANT: La Thangue, Nicholas B APPLICANT: Bandara, Lesantha R TITLE OF INVENTION: Peptide antagonists of DP transcription factors FILE REPERENCE: 620-67 CURRENT APPLICATION NUMBER: US/09/308,935 CURRENT FILING DATE: 1999-05-27 EARLIER APPLICATION NUMBER: PCT/GB97/03506 EARLIER APPLICATION NUMBER: DS/05-20 EARLIER APPLICATION NUMBER: D9 636589.7 EARLIER APPLICATION NUMBER: D9 56589.7 EARLIER PILING DATE: 198-12-20 SOTWHARE: PATENTIN VOI: 2.1 PEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-1 RESULT 1 US-09-308-935-1 TYPE: PRT ORGANISM: Artificial Sequence surgial start

Length 37; Indela

Gaps

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RESULT 3 Claims ON AT US-08-428-131-11
GENERAL INFORMATION:

APPLICANT: La Thanque, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS;
ADDRESSEE: Nixon 6 Yanderhye
STREET: 1100 NO. 5863757th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
IIP: 22201-4714
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5863757
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DS-09-078-596-11
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Best Local Similarity 100.
Matches 37; Conservative
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 3-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ARTHUR R. CRAWFORD
REGISTRATION UNMBER: 15,37
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEFAR: (703) 816-4100
TELEFAR: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTMARS: PACENTIN Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION MOMBER: US/08/428,131
FILING DATE: 23-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                    CONFUTER READABLE FORM:

#EDITOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTMARE: Pacentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDIUM TYPE: Floppy disk
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LE OP INVENTION: Transcription Factor DP-1
RR OF SEQUENCES: 14
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1100 No. 6150116th Glebe Road, Bth Floor
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us-09-078-596-11 protein
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Best Local Similarity 100.0%;
Matches 37; Conservative C
                                                                   Ouery Match 100.0%; Score 186; DB 3; Best Local Similarity 100.0%; pred, No. 2.3e-20; Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: GB 9610195.1
APPLICATION NUMBER: GB 9610195.1
APPLICATION NUMBER: GB 9610195.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                  TELECONMUNICATION INFORMATION:
TELEPHONE: 703-815-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                             WOLECULE TYPE: protein
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IPPLICARY: deLaluna, Susana

ITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOPORMS

ITLE OF INVENTION: THEREOP
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TOPOLOGY: 'linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KNIRRRYYDALWYLWWNIISKEKKEIRWIGLPTNSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-8EP-1996
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1100 NO. 5859199th Glebe Rd. 8th floor
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deLaluna, Susana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.30
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Pred. No. 3e-21;
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RESULT 5 US-08-723-415B-11 ; Sequence 11, Application US/08723415B

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; MOLECULE TYPE: protein US-08-723-4158-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             equence 2, Application US/08428131
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SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TYPE: amino acid
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MEDIUM TYPE: Floppy dish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: LICE
STREE
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PALENTIN RAIJAGGG #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TTLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TTLE OF INVENTION: THEREOF
MBER OF EXQUENCES: 21
IRRESPONDENCE ADDRESS: ADDRESSE: NIXON & VANDERHYP A CAPPESSEE: NIXON & VANDERHYP A
                                                MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPUTER: DC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25 (EPO)
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STATE: VA
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TLE OF INVENTION: Transcription Factor DP-1
MBER OF SEQUENCES: 14
RRESPONDENCE ADDRESS:
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APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2: Nixon & Vanderhye
1100 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB 9510195.1
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; MOLECULE TYPE: protein US-08-428-131-2
US-08-602-846-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-602-846-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 186; DB 2; Best Local Similarity 100.0%; Pred. No. 2.3e-20; Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703) 816-410
NEORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quence 2, Application US/08602846 cent No. 5871901
                                                                                                                                                                                                                                                                                                                     EIP: 22201-4714
COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: mmino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               DDRESSEE:
                                          amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                 8: Nixon & Vanderbye PC
9th Ploor, 1100 No. 5871901th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LA Thangue, Nicholas B
VENTION: ASSAT FOR INHIBITORS OF DP-1 AND OTHER DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-1995
                                                                                                                                                                                                                                              US/08/602,846
                                                                                                                                                    620-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Longth 410:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>.</u>
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Query Match 100.0%; Score 186; DB 2; Best Local Similarity 100.0%; Pred. No. 2.3e-70; Matches 37; Conservative 0; Mismatches 0;

Length 410;

Indels

0

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WOLECULE TYPE: protein US-09-078-596-2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Overy Match 100.0%; Score 186; DB 4; Length 410; Best Local Similarity 100.0%; Pred. No. 2.3e-246.
Natches 37; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09078596
Pacant No. 6150116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: U5/08/428,131
FILING DATE: 23-UUN-1995
ATTORNET/AGENT INFORMATION:
NAME: ATTON T. Crawford
REGISTATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
               CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR PILING DATE: 1995-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR PILING DATE: 1995-05-15
                                                                                                                                                                                                                                                                             09-189-627A-10
                                                                                                                                                                                                                                 Tent No. 6159691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAtentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
ORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon '''
STREET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 816-4100 POR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                            TILE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
                                                                                                                                                                                                                                                                                                                                                       STATE: Virginia
                                                                                                                                                                                                                      NEORMAT
                                                                                                                                                                         de la Luna, Susana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1100 No. 6150116th Glebe Road, 8th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Caps
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COMPUTER READABLE FORM:
RECOIDM TYPE: FICAPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  PPLICANT: deLaluna, Súsana
ITLE OF INVENTION: TRANSCR
ITLE OF INVENTION: THEREOF
                                                                                                                                                              CITY: Arlington
STATE: VA
                                                                                                                                                                                                                      DDRESSEE:
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pplication US/D8723415B

1100 No. 5859199th Glebe Rd.

8th floor

TRANSCRIPTION PACTOR DP-3 AND ISOFORMS

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; TYPE: PRT
; ORGANISM: mouse
US-09-189-627A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 100.0% Score 186; DB 4; Best Local Similarity 100.0% Pred. No. 2.3e-20; Matches 37; Conservative 0; Mismatches 0;
                                                                     Query Match 100.0%; Score 186; DB 4; Best Local Similarity 100.0%; Pred. No. 2.3e-20; Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEO ID NO 10
                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: GB 9 PRIOR PILING DATE: 1996-05-1* NUMBER OF SEA
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/189,627A CURRENT FILING DATE: 1998-11-10 PRIOR APPLICATION NUMBER: 08/723,415 PRIOR FILING DAYE: 1996-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-189-627A-11
                                                                                                                                                                                                                                                                                                                                                                                                                           quence 11, Application US/09189627A
Cent No. 6199691
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                                                                                                                                                                                                                                                                                                                                                                                            La Thangue, Nicholas
                                                                                                                                                                                                                                                       UMBER: GB 9610195
1996-05-15
                                                                                                                                                                                                                                                                                                                                                                  TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 410;
                                                                                                  Length 410;
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                                                                        Caps
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APPLICATION NUMBER: US/08/723,4158 FILING DATE: 30~5EP-1996

APPLICATION DATA:

GB 9610195.1

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7 ORGANISM: mouse
US-09-189-627A-4
                                                                                                                                                                                                                                                         Ouery Match 97.8%; Score 182; DE 4; Length 369; Best Local Similarity 97.3%; Pred. No. 8.4e-20; Matches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REPERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 1996-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-189-627A-4
                                                                                                                                                                                   PPLICART: LaThangue, Nicholas B.
PPLICART: DéLaluns, Susana
(TLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
(TLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB of PILING NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4, Application US/09189627A
6, 6159691
                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn
                                                                                                     Application US/087234158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Le Thangue, Nicholas
de la Luna, Susana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MBER: GB 9610195
1996-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08/723,415
                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                       Cape
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Overy Match 97.8%, Score 182; D8 4 Length 370; Best LOCal Similarity 97.3%; Pred. No. 8.4e-20; Natches 36; Conservative 1; Mismatches 0; Indels

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; ORGANISM: mouse
US-09-189-627A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-723-415B-6
                                                                                                                                                                                                                                                                                                                                                   US-09-189-627A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.8%;
Best Local Similarity 97.3%;
Matches 36; Conservative
                                                    LENGTH: 3
                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09189627A
Patent No. 6159691
                                                                                                                                                                                                                                                                             GENERAL INFORMATI
APPLICANT: LA T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: GB 9610195.1
PILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: CTAVEOID, AICHUI R.
REGISTRATION NUMBER: 25.327
REFERENCE/DOCKET NUMBER: 117-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEPAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 6: \
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/723,4158
FILING DATE: 30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                       102 EMIRRRYYDALNYLMAMNIISKEKKEIKHIGLPTNSA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: NIXON
STREET: 1100 NO.
CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KNIRRRYYDALHYLAMNIISKEKKEIKWIGLPINSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22201-4741
                                                    370
                                                                                                                                                                                                                                                          La Thangue, Nicholas
de la Luna, Susans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1100 NO. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                          oppy disk
                                                                                                                                                                                                                                            TRANSCRIPTION FACTOR DP-3 AND ISOPORMS THEREOF
                                                                                                                                                                                        MBD: US/09/189,627A
1998-11-10
                                                                                                                                                                    08/723,415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 182;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 6.4a-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Query Match Best Local Similarity Matches 36; Conserv

97.8%; Score 182; DB 2; Length 369; Ilerity 97.3%; Pred. No. 8.4e-20; Conservative 1; Mismatches 0; Indels

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
NFORMATION FOR SEQ ID NO: 4: V

NAME: Crawford, Arthur R. REGISTRATION NUMBER: 25,327 REPERENCE/DOCKET NUMBER: 11

17-220

SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Page 6

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: TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-723-4158-8
                                                                      Overy Match 97.8%; Score 182; DB 2; UBest Local Similarity 97.3%; Pred. No. 8.8e-20; Matches 36; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 2201-4741

COMPUTER READABLE FORM:

MEDIGN TYPE: Ploppy disk

COMPUTER: EIBH PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: nc nn /723.415B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
TTORNEY/AGENT INFORMATION:
NAME: Crawford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: NIXON & VANDERHYE P.C.
STREET; 1100 No. 5859199th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAL INPORMATION:
PLICANT: LaThangue, Nicholas B.
PLICANT: deLaluna, Susans
TLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                          NME: Crawford, Arthur R.
EGISTRATION NUMBER: 25,327
EFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPPLICATION NUMBER: US/08/723,415B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ge 8. Application US/087234158
No. 5859199
                                                                                                                                                                                                                                                                                                                                                      COMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                        117-220
                                                                                                             Length 385;
                                                                           Indels
                                                                           0; Caps
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Search completed: August 28, 2002, 12:59:33 Job time: 144 sec

Limitaria

Run on: OM protein .

12. Appl 12. Appl 12. Appl 13. Appl 14. Appl 13. Appl 13. Appl 14. Appl 14. Appl 14. Appl 14. Appl 15. Appl 16. Appl 17. Appl 18. Appl 18. Appl

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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-900-147-1
186
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                                                                                                                                                                                                                                                                                                                                                                                  888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNIRRRVYDALNVLMANNIISKEKKEIKWIGLPTNSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/BCMB.COMB.pep:*
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(c) 1993 - 2000 Compugen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search time 12.99 Seconds (without alignments) 69.573 Million cell updates/sec
                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; is Best Local Similarity 100.0%; is Matches 37; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/308,915
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: PCT/GB97/0306
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: GB 9626589.7
EARLIER FILING DATE: 1996-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICARY: Bandara, Lasantha R
TITLE OF INVENTION: Peptide entagonists of DP
FILE REFERENCE: 620-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                  TITLE OF INVENTION: TINUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS
                                 ADDRESSEE:
STREET: 1:
CITY: Arlington
STATB: Virginia
                                                                                                                                                                                                                                                       1 KNIRRRYTDALNYJAMONI SKEKKEIKMIGLPTNSA 37
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                                                                                                                                                                       Application US/08428131
                                                                                                                                                                                                        dis ost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thangue, Nicholas B
                                                                                                   LA Thangue, Nicholas Barrie
PENTION: Transcription Pactor DP-1
                                   Nixon & Vanderhye
00 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                 Score 186; DB 4;
Pred. No. 1.3e-21;
No. Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription factors
                                                                                                                                                                                                                                                                                                                                                                   Length 37;
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Query Natch 100.0 Best Local Similarity 100.0 Marches 37, Conservative
                                             APPLICATION NOMBER: US/08/428,131
PILLING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
                                                                                                                                                                                          SOTTWARE: Patentin Release #1.0, Version #1.35 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
FILING DATE:
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
                                                                                                                                                  RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
             TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            PLICANT: La Thangue, Nicholas Barrie
FIE OF ENVENTION: Transcription Factor DP-1
BER OF SEQUENCES: 14
RESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 KNJRRVYDALNYLMANNIISKEKKEIKHIGLPINSA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KNIRRRYYDALMYLMUNIISKEKKEIKNIGLPINSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                            DRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPUTER: IBM PC compatible
STRAFING STOTEM: PC-DOS/NS-DOS
PTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Arthur R. Craw!
ISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/090785
                                                                                                                                                                                                                                                                                                                                                                                                    1100 No. 6150116th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703) 816-4000
(703) 816-4100
OR SEO ID NO: 11:
(703)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 186; DB 2
100.0%; Pred. No. 3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/428, 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Wismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>..</u>
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; TOPOLOGY: linear; HOLECULE TYPE; protein US-08-723-4198-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                         REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 11
TELECOMOUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOPTWARE: PATENTIN RAIL CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: GB 9610195.1
                                                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/723,4158 FILING DATE: 30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KNIRRRVYDALNVLMAMNIISKEKKBIRNIGLPINSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           watch Match 100.0%; Score 186; DB 4; Length 72; Local Similarity 100.0%; Pred. No. 3e-21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KHIRREYDALNVIMMNIISKEKKEIKNIGLPINSA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOPORMS
E OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08723415B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2: NIXON 4 VANDERHYB P.C.
1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LaThangue, Nicholas B.
                                                                                                                                                                                                                                                                                 Arthur R
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Sequence 11, Application 05/097234158

Watch 100.0%; Local Similarity 100.0%; local Similarity 100.0%; les 37; Conservative 0

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Score 186; DB 2; Pred. No. 2.3e-20; Nismatches 0;

Length 410; Indels

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COMPUTER READARLE FORM:
COMPUTER READARLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IM PC compatible
COMPUTER: IM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS:
OPERATING SYSTEM: POSITION SYSTEM:
APPLICATION MUMBER: US/08/723,415B
FILING DATE: 00-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 100.0%; Score 186; DB 2; Best Local Similarity 100.0%; Pred. No. 2.3e-20; Vatches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-428-131-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-816-4100
NFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                         COUNTRY: U.S.A.

IIP: 2201-4714
COMPUTER READABLE FORM:
REDUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: GB 9610195.1
PILLED DATA:
APPLICATION NUMBER: GB 9610195.1
PILLED DATE: 13-MAY-1996
PILLED DATE: 13-MAY-1996
ATTORNET/AGENT REPORMATION:
                                                                                                                                                                                                                                                                   APPLICANT: La Thangue, Micholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
MINIBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: procein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: CREWford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE, DOCKET NUMBER: 117-220
FELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TRANSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 NG
CITY: Arlington
STATE: Virginia
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STREET: 1100 No. 5859199th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 410 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                        Addressee:

    Application US/08428131
    5863757

                                                                                                                                                                                                                         1100 No. 5863757th Glabe Road, 8th Floor
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deLaluna, Susana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
  Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
Overy Match 100.0%; Score 186; DB; Best Local Similarity 100.0%; Pred. Mo. 2.38-20; Matches 37; Conservative 0; Mismatches 0.
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US-08-602-846-2
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WOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 186; DB 3; Best Local Similarity 100.0%; Pred. No. 2.3e-20; Matches 37; Conservative 0; Mismatches 0;
                                                                                                  TELEFAX: (703) 816-410
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CRANFORD, ARTHUL R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PATENTION ROLL
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy dish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 KNIRRRYYDALMYLMAMNIISKEKKEIKWIGLPTHSA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
STATE: Virginia
                               TYPE: 410 amino acids
TYPE: amino acid
TOPOLOGY: 1'-
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KNIRRRYYDALNYLAAMNIISKEKKEINWIGLPTHSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/428,131 FILING DATE: 23-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 11
LECOMMUNICATION INFORMATION:
PELEPHONE: (703) 815-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LICANT: La Thangue, Wicholas B
LE OF INVENTION: ASSAY FOR INHIBITORS OF DP-1 AND OTHER DP
LE OF INVENTION: PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Application US/08602846 5871901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2: Nixon & Vanderhye PC
8th Floor, 1100 No. 5871901th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 amino acids
                                                                                                                                                                                                                                                                                                                                                               Release #1.0
                                                                                                                                                                                                                                                                                                                          US/08/602,846
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Length 410; Indels

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SOFTWARE:

Patentin Ver. 2.0

Cength 410,

Indels

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US-09-078-596-2
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Best Local Similarity 100.
Atches 37; Conservative
                                                                                                                                                                                                                                                                              09-189-627A-10
PPLICAT: La Thangue, Nicholas

PPLICAT: de la Luna, Susana

PPLICAT: de la Luna, Susana

PPLICAT: de la Luna, Susana

ILE REFERENCE: 620-54

URRENT APPLICATION NUMBER: U5/09/189,627A

URRENT FILING DATE: 1998-11-10

RIOR APPLICATION NUMBER: 08/723,415

RIOR FILING DATE: 1996-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTMARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 816-4100
ORNATION FOR SEQ ID MO: (
EQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/078,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNIRRRYTDALHYLMAMNIISKEKKEIKWIGLPTNSA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application 05/09078596
                                                                                                                                                                                                                                                       Application US/09189627A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2: Nixon & Vanderhye
1100 No. 6150116th Glebe Road, Bth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          La Thangue, Nicholas Barrie
ENTION: Transcription Factor DP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 186; DB 4; Length 410; 100.0%; Pred. No. 2.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/428, 131
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US-09-189-627A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE, 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                     equence 4, Application at ent No. 5859199 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 KNIRRRYYDALNYLMANNIISKEKKEIKNIGLPTNSA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 KNIRRVYDALNVLMAMNIISKEKKEIKNIGLPTNSA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KNIRRRYYDALNYLJUNNIISKEKKEIKWIGLPINSA 37
                                                              MEDION TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KNIRRRYYDALNYLMANNIISKEKKEIKWIGLPINSA 37
                                                                                                                                                                                                        DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/189,627A FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                         INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                             Application US/08723415B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  La Thangue, Nicholas
de la Luna, Susana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09189627A
                                                                                                                                                                                    B: NIXON & VANDERHYE P.C.
1100 No. 5859199th Glebe Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 186; DB 4;
100.0%; Pred. No. 2.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 186; DB 4; 100.0%; Pred. No. 2.3e-20
  elease #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                   Nicholbs 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB 9610195.
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Length 410;

Indels

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Sp G

8th floor

APPLICATION NUMBER:

UMBER: US/08/723,415B 30-SEP-1996

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US-09-189-627A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.8%;
Best Local Similarity 97.3%;
Matches 36; Conservative
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-189-627A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELECOMMUNICATION INFORMATION
                                                                                                                                                                O) ENTRERVYDALNVLMAMNIISKEKKEIKWIGLPTNSA 137
                                                                                                                                                                                                                         Local Similarity 97.
                                                                                                                                                                               1 KNIRRRYYDALNYLJAANNIISKEKKEIKWIGLPINSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ME: Crawford, Arthur R. GISTRATION NUMBER: 25,327 FERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/189,627A FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09189627A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              La Thangue, Nicholas
de la Luna, Susana
                                                                                         pplication US/08723415B
LaThangue, Nicholas B.
delaluna, Subana
Tention: Therbop
Tention: Therbop
                                                                                                                                                                                                                                                                                                                                                                                                                                        ION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                          1996-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                          1996-09-30
                                                                                                                                                                                                                                     97.8%; Score 182; DB 4; 97.3%; Pred. No. 8.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB 9610195.1
                                                                                                                                                                                                                                                                                                                                                                                                                           GB 9610195
                                                                                                                                                                                                                                                                                                                                                                                                                                                       08/723,415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 182; DB 2;
Pred. No. 8.4e-20;
1; Mismatches 0
                                                                                                                                                                                                                                                    DB 4; Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                         Indels
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Query Natch
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM;
MEDIOM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                        LECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/723,419B FILING DATE: 30-SEP-1996
                                                                                                                                                                Application US/09189627A
                                                                                                Le Thengue, Nicholes
de la Luna, Susana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: NIXON & VANDERBYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                    370 amino acida
                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                      Transcription factor DP-3 and isoforms thereop
                                                                                                                                                                                                                                                                                                                   97.8%;
97.3%;
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                                                        US/09/189, 627A
GB 9610195
                                                                                                                                                                                                                                                                                                                 Score 182; DB 2;
Pred. No. 8.4e-20;
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                                                                                                                                                                                                                                                                                                                                Length 370;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                     0, Caps
                                                                                                                                                                                                                                                                                                     0
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Query Match
Best Local Similarity 97.,
36; Conservative

DB 4; Length 370;

Indels

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us-09-900-147-1.rai
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; TOPOLOGY: linear; HOLECULE TYPE: protein US-08-723-4158-8
                                                                         Query Match 97.8%; Score 182; DB 2; L est Local Similarity 97.3%; Pred. No. 8.8e-20; Astches 36; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentin Release #1.0. Version #1.30

CURRENT APPLICATION DATA:

APPLICATION HUMBER: US/08/723.415B

FILING DATE: 30.8EP-1996

CLASSIFICATION DATA:

APPLICATION MUMBER: GB 9610195.1

FILING DATE: 15-MAY-1996

ATTORNEY/AGENT INFORMATION:

NUMBER/AGENT INFORMATION:
STREET: 1100 No.
CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS 
E OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Application US/087234158 5859199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: NIXON & VANDERHYE P.C.
1100 No. 5859199th Glebe Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AThangue, Nicholas B.
                                                                                                                                                                                                                                                                                                                                                                       17-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8th floor
                                                                                                               Length 385;
                                                                           Indels
                                                                         0
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Search completed: August 28, 2002, 12:59:33 Job time: 144 sec